

QY 421 CTGTCAATAGCAGAGTGCATGTTGGAATGTCGCGCGTCAATGTTAGATATGCAAGC 480
| | | | |
DB 421 CTGTCAATAGCAGAGTGCATGTTGGAATGTCGCGCGTCAATGTTAGATATGCAAGC 480
QY 481 GAAGGCCAACCAATGATCTTGAAACTTTGGAAAATGATACAAAACAAAACAGAGCA 540
| | | | |
DB 481 GAAGGCCAACCAATGATCTTGAAACTTTGGAAAATGATACAAAACAAAACAGAGCA 540
QY 541 TTATTAATCTTTGGCGTTATAGTGCAGACAGATATCGCTAATGTCGATGATCACTTAA 600
| | | | |
DB 541 TTATTAATCTTTGGCGTTATAGTGCAGACAGATATCGCTAATGTCGATGATCACTTAA 600
QY 601 GAACATTTAGAAAGTTATGATTTATGATTTAGTATGTTCCAGATTAAGATGATTTA 660
| | | | |
DB 601 GAACATTTAGAAAGTTATGATTTATGATTTAGTATGTTCCAGATTAAGATGATTTA 660
QY 661 TTAGACTGCTATGCTGATGAAAGCAAGTTAGTAAAAAAGTGGCAGCGATCTTGAAAT 720
| | | | |
DB 661 TTAGACTGCTATGCTGATGAAAGCAAGTTAGTAAAAAAGTGGCAGCGATCTTGAAAT 720
QY 721 AATTAAGTACGTACGTGAGTTTATAGGGAAGATGCGCAGAAATTAATGATTTAT 780
| | | | |
DB 721 AATTAAGTACGTACGTGAGTTTATAGGGAAGATGCGCAGAAATTAATGATTTAT 780
QY 781 CATAGAGACGACGATGATGAACTAACGCAATTTGATGAACTCAATACAAAACAC 840
| | | | |
DB 781 CATAGAGACGACGATGATGAACTAACGCAATTTGATGAACTCAATACAAAACAC 840
QY 841 TTATTAGAAATCGTTGATTTA 861
| | | | |
DB 841 TTATTAGAAATCGTTGATTTA 861

RESULT 2
US-09-134-001C-334
; Sequence 334, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 334
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-334

Query Match 2.9%; Score 25; DB 4; Length 909;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAGGAAATTAACAATCATTAAGT 305
| | | | |
DB 308 GAGGAAATTAACAATCATTAAGT 332

RESULT 3
US-09-484-970B-110
; Sequence 110, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmutz, Wayne
; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 110
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 009051.5CB1
US-09-484-970B-110

Query Match 2.1%; Score 18; DB 4; Length 763;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GATGAATTAATTAATGA 32
| | | | |
DB 212 GATGAATTAATTAATGA 229

RESULT 4
US-07-686-322A-1
; Sequence 1, Application US/07686322A
; Patent No. 5312733
; GENERAL INFORMATION:
; APPLICANT: MacLeod Dr., Carol L.
; TITLE OF INVENTION: No. 5312733el T-cell lymphoma cDNA clones
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department, Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/686,322A
; FILING DATE: 19910411
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/509684
; FILING DATE: 13-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauener, Charlene A.
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: D-5232-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-3634
; TELEFAX: (713) 651-5246
; TELEX: Western Union 762829
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1301 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: AKR1 Jackson
; INDIVIDUAL ISOLATE: SL12 cell line
; TISSUE TYPE: Lymphoma
; CELL TYPE: T-cell
; CELL LINE: SL12.3 and SL12.4

IMMEDIATE SOURCE:
CLONE: 19.1
US-07-686-322A-1

Query Match 2.1%; Score 18; DB 1; Length 1301;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CAATACAAAACCTTATT 845
DB 3 CAATACAAAACCTTATT 20

RESULT 5

US-08-002-999-1
Sequence 1, Application US/08002999
Patent No. 5440017
GENERAL INFORMATION:
APPLICANT: Macleod Dr., Carol L.
TITLE OF INVENTION: No. 5440017el T-cell lymphoma cDNA clones
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department, Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,999
FILING DATE: 19930111
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,322
FILING DATE: 11-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D-532-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5587
TELEFAX: (713) 651-5246
TELEX: Western Union 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: AKR1 Jackson
INDIVIDUAL ISOLATE: SUI2 cell line
TISSUE TYPE: Lymphoma
CELL TYPE: T-cell
CELL LINE: SUI2.3 and SUI2.4
IMMEDIATE SOURCE:
CLONE: 19.1
US-08-002-999-1

Query Match 2.1%; Score 18; DB 1; Length 1301;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CAATACAAAACCTTATT 845
DB 3 CAATACAAAACCTTATT 20

RESULT 6
US-08-700-651-1
Sequence 1, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 5163
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-08-700-651-1

Query Match 2.1%; Score 18; DB 3; Length 5163;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCATGATCTTGAACCT 507
DB 3769 CCATGATCTTGAACCT 3786

RESULT 7

US-08-928-361B-4
Sequence 4, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VERNY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-928-361B-4

Query Match 2.1%; Score 18; DB 3; Length 5163;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507
DB 3769 CCAATTGATCTTGAACACT 3786

RESULT 8

US-09-588-995A-4
Sequence 4, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 5163
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-4

Query Match 2.1%; Score 18; DB 4; Length 5163;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507
DB 3769 CCAATTGATCTTGAACACT 3786

RESULT 9

US-08-700-651-2
Sequence 2, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAs AND RNAs
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-08-700-651-2

Query Match 2.1%; Score 18; DB 3; Length 5318;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507
DB 3769 CCAATTGATCTTGAACACT 3786

RESULT 10

US-08-928-361B-3
Sequence 3, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-928-361B-3

Query Match 2.1%; Score 18; DB 3; Length 5318;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATTGATCTTGAACACT 507
DB 3769 CCAATTGATCTTGAACACT 3786

RESULT 11

US-09-588-995A-3
Sequence 3, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 5318
TYPE: DNA
ORGANISM: Cryptosporidium parvum
US-09-588-995A-3

Query Match 2.1%; Score 18; DB 4; Length 5318;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 CCAATGATCTTGAAGT 507
DB 3769 CCAATGATCTTGAAGT 3786

RESULT 12
US-09-702-705-1416
Sequence 1416, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1416
LENGTH: 540
TYPE: DNA
ORGANISM: Homo sapien
US-09-702-705-1416

Query Match 2.0%; Score 17; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 AAGTAAATAAAGTT 411

DB 522 AAGTAAATAAAGTT 538

RESULT 13
US-09-736-457-1416
Sequence 1416, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1416
LENGTH: 540
TYPE: DNA
ORGANISM: Homo sapien
US-09-736-457-1416

Query Match 2.0%; Score 17; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 AAGTAAATAAAGTT 411
DB 522 AAGTAAATAAAGTT 538

RESULT 14
US-09-385-982-404
Sequence 404, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 404
LENGTH: 604
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(604)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-404

Query Match 2.0%; Score 17; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTCAGCTAGAGAAAGT 99
 Db 289 CTCAGCTAGAGAAAGT 305

RESULT 15

US-09-385-982-173
 ; Sequence 173, Application US/09385982
 ; Patent No. 6262334
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDEGE, WILSON O., ET AL.
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; FILE REFERENCE: CCDNA-260XX
 ; CURRENT APPLICATION NUMBER: US/09/385,982
 ; EARLIER FILING DATE: 1999-06-30
 ; EARLIER APPLICATION NUMBER: 09/328,111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: 60/117,393
 ; EARLIER FILING DATE: 1999-01-27
 ; EARLIER APPLICATION NUMBER: 60/098,639
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 544
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 173
 ; LENGTH: 616
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(616)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-385-982-173

Query Match 2.0%; Score 17; DB 3; Length 616;
 Best Local Similarity 100.0%; Pred.No. 50;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 CTCAGCTAGAGAAAGT 99
 Db 286 CTCAGCTAGAGAAAGT 302

Search completed: November 29, 2003, 17:03:58
 Job time : 76 secs

QY	1	ATGACGATCTACCGATGCAATTAATTAATAGTAGAGTCAATAATGAATTAATCGGTGG	60
Db	1	ATGACGATCTACCGATGCAATTAATTAATAGTAGAGTCAATAATGAATTAATCGGTGG	60
QY	61	ATAAATAAATCAGTAATGAGTACTCAGCTAGAGAAAGATGTTGATTCATTTAAATGCT	120
Db	61	ATAAATAAATCAGTAATGAGTACTCAGCTAGAGAAAGATGTTGATTCATTTAAATGCT	120

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QY 121 GGAGTAAAGCAGCCAGCAGTCTGTATTAATCACTTAAGATGCAATAACCGAG 180
DB 121 GGAGTAAAGCAGCCAGCAGTCTGTATTAATCACTTAAGATGCAATAACCGAG 180
QY 181 TATGAGTTAGGTATGAAGAGCGCAATGCACTAGAAATGATCAATATTCATTATT 240
DB 181 TATGAGTTAGGTATGAAGAGCGCAATGCACTAGAAATGATCAATATTCATTATT 240
QY 241 CAGATGACCTACAGAGATGATTAATGATTAATGAGAGAAATTAACAAATCAT 300
DB 241 CAGATGACCTACAGAGATGATTAATGATTAATGAGAGAAATTAACAAATCAT 300
QY 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GAACTTATTTCAAGTATGATGATTAATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAACTTATTTCAAGTATGATGATTAATGATGATGATGATGATGATGATGATGAT 420
QY 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGAAATGATGATGATGATGATGATGATGAT 540
DB 481 GAAGGCCAACCAATTGATCTTGAACCTTGAAATGATGATGATGATGATGATGATGAT 540
QY 541 TTATTAATCTTTCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TTATTAATCTTTCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAACATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GAACATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TTGAGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TTGAGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CATAGAGACGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CATAGAGACGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
DB 841 TTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861

```

RESULT 2

```

US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P8515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63
; LENGTH: 861
; TYPE: DNA

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ORGANISM: Staphylococcus aureus
US-10-084-205-63

Query Match 100.0%; Score 861; DB 14; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCAATCTACCGATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 60
DB 1 ATGACCAATCTACCGATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 61 ATTAATTAATCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 ATTAATTAATCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 GGAGTAAAGCAGCCAGCAGTCTGTATTAATCACTTAAGATGCAATAACCGAG 180
DB 121 GGAGTAAAGCAGCCAGCAGTCTGTATTAATCACTTAAGATGCAATAACCGAG 180
QY 181 TATGAGTTAGGTATGAAGAGCGCAATGCACTAGAAATGATCAATATTCATTATT 240
DB 181 TATGAGTTAGGTATGAAGAGCGCAATGCACTAGAAATGATCAATATTCATTATT 240
QY 241 CAGATGACCTACAGAGATGATTAATGATTAATGAGAGAAATTAACAAATCAT 300
DB 241 CAGATGACCTACAGAGATGATTAATGATTAATGAGAGAAATTAACAAATCAT 300
QY 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 GAACTTATTTCAAGTATGATGATTAATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAACTTATTTCAAGTATGATGATTAATGATGATGATGATGATGATGATGATGAT 420
QY 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GAAGGCCAACCAATTGATCTTGAACCTTGAAATGATGATGATGATGATGATGATGAT 540
DB 481 GAAGGCCAACCAATTGATCTTGAACCTTGAAATGATGATGATGATGATGATGATGAT 540
QY 541 TTATTAATCTTTCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TTATTAATCTTTCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAACATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GAACATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TTGAGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TTGAGCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 AATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CATAGAGACGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CATAGAGACGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
DB 841 TTATTAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861

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RESULT 3

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US-08-781-986A-155/c
; Sequence 155, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:

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;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 2822
;; LENGTH: 413
;; TYPE: DNA
;; ORGANISM: Staphylococcus aureus
US-09-815-242-2822

Query Match 48.0%; Score 413; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 4,6e-193;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 TTGATTCTAATAATCCGAGTATGAGTATGAGGAGCGCAATTGCACTAGAAATG 219
DB 413 TTGATTCTAATAATCCGAGTATGAGTATGAGGAGCGCAATTGCACTAGAAATG 354
QY 220 ATTCAATACATATTCATTATTCATGATGACCTACAGCGATGATATGATATGCA 279
DB 353 ATTCAATACATATTCATTATTCATGATGACCTACAGCGATGATATGATATGCA 294
QY 280 CGAGGAAATTAACAATCATTAAGTATGATGAGTGAAGTGGATATTAAGAGGTAT 339
DB 293 CGAGGAAATTAACAATCATTAAGTATGATGAGTGAAGTGGATATTAAGAGGTAT 234
QY 340 GCTTTTAACTAAAGATTTGAAGTATTTCAAGTATGATATTAAGTATTAAGTAA 359
DB 233 GCTTTTAACTAAAGATTTGAAGTATTTCAAGTATGATATTAAGTATTAAGTAA 174
QY 400 AAAATTAAGTTTACACAGCGCTGTCAATAGCAAGTGTATGTAATGTCGGCGGT 459
DB 173 AAAATTAAGTTTACACAGCGCTGTCAATAGCAAGTGTATGTAATGTCGGCGGT 114
QY 460 CAAATGTATGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATA 519
DB 113 CAAATGTATGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATA 54
QY 520 CACAAAACAAAACAGAGGATTTAATTAATTTGCGGTTATGATGAGAGAGA 572
DB 53 CACAAAACAAAACAGAGGATTTAATTAATTTGCGGTTATGATGAGAGAGA 1

RESULT 7
US-09-815-242-3275/C
; Sequence 3275, Application US/09815242
; Patent No. US2002006159A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578

;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 3275
;; LENGTH: 337
;; TYPE: DNA
;; ORGANISM: Staphylococcus aureus
US-09-815-242-3275

Query Match 39.1%; Score 337; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TACATATTCATTTATTCATGATGACCTACAGGATGATATGATATGATGACGAGG 284
DB 337 TACATATTCATTTATTCATGATGACCTACAGGATGATATGATATGATGACGAGG 278
QY 285 AAAATTAACAATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 344
DB 277 AAAATTAACAATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 218
QY 345 ATTAATTAAGCATTTGAACCTATTTCAAGTATGATGATGATGATGATGATGATGAT 404
DB 217 ATTAATTAAGCATTTGAACCTATTTCAAGTATGATGATGATGATGATGATGATGAT 158
QY 405 AAAAGTTTACACAGCGCTGTCAATAGCAAGTGTATGTAATGTCGGCGGTAAAT 464
DB 157 AAAAGTTTACACAGCGCTGTCAATAGCAAGTGTATGTAATGTCGGCGGTAAAT 98
QY 465 GTTAGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATATACAA 524
DB 97 GTTAGATATGCAAGCGCAAGCGCAACCAATGATTTGAACTTTGAAATGATATACAA 38
QY 525 AACAAAACAGAGCATTTTAACTTTTGGCGTTANG 561
DB 37 AACAAAACAGAGCATTTTAACTTTTGGCGTTANG 1

RESULT 8
US-09-864-761-24950/C
; Sequence 24950, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664


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/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 194294
/ LENGTH: 580
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-194294
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Query Match 2.2%; Score 19; DB 13; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 394 GAAGTAAATAAAGTTC 412
Db 85 GAAGTAAATAAAGTTC 103
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RESULT 12

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US-10-027-632-194295
/ Sequence 194295, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827,129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 194295
/ LENGTH: 580
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-194295
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Query Match 2.2%; Score 19; DB 13; Length 580;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 394 GAAGTAAATAAAGTTC 412
Db 85 GAAGTAAATAAAGTTC 103
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RESULT 13

US-09-864-761-8212/c

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/ Sequence 8212, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aeomica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 8212
/ LENGTH: 600
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AL117667.2
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.7
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
US-09-864-761-8212
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Query Match 2.2%; Score 19; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 503 AACCTTGGAATGATACA 521
Db 470 AACCTTGGAATGATACA 452
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RESULT 14

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US-10-027-632-21738
; Sequence 21738, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21738
; LENGTH: 922
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-21738
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Query Match      2.2%; Score 19; DB 12; Length 922;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      299 ATAAAGTATATGTTGAGTG 317
DB      803 ATAAAGTATATGTTGAGTG 821
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RESULT 15

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US-10-027-632-21739
; Sequence 21739, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21739
; LENGTH: 922
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-21739
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Query Match      2.2%; Score 19; DB 12; Length 922;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      803 ATAAAGTATATGTTGAGTG 821
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 12:31:54 ; Search time 72 Seconds

(without alignments)
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Title: US-09-925-637-63

Sequence: 1 atgacgaactaccgatgaa.....tattagaatcgttgattca 861

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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seg: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	Query DB ID	Description
1	853	99.1	882 3 US-09-276-873-1	Sequence 1, Appl1
2	449.8	52.2	909 4 US-09-134-001C-334	Sequence 334, Appl
3	160.4	18.6	939 4 US-09-107-532A-3070	Sequence 3070, Ap
4	157.2	18.3	894 1 US-08-534-910B-5	Sequence 5, Appl1
5	155.6	18.1	893 1 US-08-333-321-1	Sequence 1, Appl1
6	155.6	18.1	894 1 US-08-534-910B-2	Sequence 2, Appl1
7	155.6	18.1	894 1 US-08-534-910B-3	Sequence 3, Appl1
8	155.6	18.1	894 1 US-08-534-910B-4	Sequence 4, Appl1
9	155.6	18.1	894 3 US-08-886-466-1	Sequence 1, Appl1
10	155.6	18.1	894 3 US-08-475-304-1	Sequence 1, Appl1
11	155.6	18.1	894 4 US-09-101-126-4	Sequence 4, Appl1
12	155.6	18.1	894 4 US-09-367-528A-4	Sequence 4, Appl1
13	154	17.9	894 4 US-08-534-910B-1	Sequence 1, Appl1
14	154	17.9	894 4 US-09-367-528A-2	Sequence 2, Appl1
15	150.6	17.5	466 3 US-09-217-609A-28	Sequence 28, Appl
16	150.6	17.5	466 3 US-08-873-235B-28	Sequence 28, Appl
17	137	15.8	885 4 US-08-916-421B-1	Sequence 1, Appl1
18	136.4	15.8	885 3 US-09-187-050-11	Sequence 11, Appl
19	134.8	15.7	1179 3 US-09-187-050-13	Sequence 13, Appl
20	134.8	15.7	1179 3 US-09-187-050-15	Sequence 15, Appl
21	134.8	15.7	1179 3 US-09-187-050-17	Sequence 17, Appl
22	134.8	15.7	1179 3 US-09-187-050-19	Sequence 19, Appl
23	134.8	15.7	1179 3 US-09-187-050-21	Sequence 21, Appl
24	134.8	15.7	1179 3 US-09-187-050-23	Sequence 23, Appl
25	134.8	15.7	1179 3 US-09-187-050-25	Sequence 25, Appl
26	134.8	15.7	1889 3 US-09-187-050-1	Sequence 1, Appl1
27	134.4	15.6	847 4 US-09-634-238-85	Sequence 85, Appl

28	131.4	15.3	1830121 4 US-09-557-884-1	Sequence 1, Appl1
29	131.4	15.3	1830121 4 US-09-643-990A-1	Sequence 1, Appl1
30	124.6	14.5	876 3 US-09-375-742-1	Sequence 1, Appl1
31	124.2	14.4	10011 4 US-08-861-527-76	Sequence 76, Appl
32	114.8	13.3	1914 4 US-09-634-238-41	Sequence 41, Appl
33	92.4	10.7	927 4 US-09-328-352-64	Sequence 64, Appl
34	76.8	8.9	1284 4 US-08-858-207A-173	Sequence 173, App
35	72.6	8.4	861 3 US-09-187-050-4	Sequence 4, Appl
36	72	8.4	909 1 US-07-783-705A-7	Sequence 7, Appl1
37	72	8.4	6918 1 US-07-783-705A-13	Sequence 13, Appl
38	71.4	8.3	990 1 US-08-410-167A-1	Sequence 1, Appl1
39	71.4	8.3	993 1 US-08-705-377-1	Sequence 1, Appl1
40	71.4	8.3	993 1 US-08-705-377-2	Sequence 2, Appl1
41	71.4	8.3	993 1 US-08-705-377-4	Sequence 4, Appl1
42	71.4	8.3	993 1 US-08-705-377-5	Sequence 5, Appl1
43	71.4	8.3	993 2 US-09-052-962-1	Sequence 1, Appl1
44	71.4	8.3	993 2 US-09-052-962-2	Sequence 2, Appl1
45	71.4	8.3	993 2 US-09-052-962-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1				
US-09-276-873-1				
; Sequence 1, Application US/09276873				
; Patent No. 6107058				
; GENERAL INFORMATION:				
; APPLICANT: Wilding, Edwina Imogen				
; APPLICANT: Gwynn, Michael				
; TITLE OF INVENTION: Ispra				
; FILE REFERENCE: GM10208				
; CURRENT APPLICATION NUMBER: US/09/276, 873				
; CURRENT FILING DATE: 1999-03-26				
; NUMBER OF SEQ ID NOS: 2				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 1				
; LENGTH: 882				
; TYPE: DNA				
; ORGANISM: Staphylococcus aureus				
US-09-276-873-1				
Query Match 99.1%; Score 853; DB 3; Length 882;				
Best Local Similarity 99.4%; Pred. No. 2.8e-198;				
Matches 856; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
QY	1	ATGACGATCTACCGATGATTAATTAATGATGAAGTCAATATGATTCGTTGCG	60	
DB	1	ATGACGATCTACCGATGATTAATTAATGATGAAGTCAATATGATTCGTTGCG	60	
QY	61	ATTAATTAATCACTAATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120	
DB	61	ATTAATTAATCACTAATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	120	
QY	121	GGAGTAAACGATCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180	
DB	121	GGAGTAAACGATCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180	
QY	181	TATGATTTAGTGTGAAGAGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240	
DB	181	TATGATTTAGTGTGAAGAGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240	
QY	241	CATGATGCTTACCGATGATTAATGATGATTAATGATGATTAATGATTAATGAT	300	
DB	241	CATGATGCTTACCGATGATTAATGATGATTAATGATGATTAATGATTAATGAT	300	
QY	301	AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360	
DB	301	AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360	
QY	361	GAATTAATTTCAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATG	420	
DB	361	GAATTAATTTCAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATG	420	


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D8      89   GGC CGCG CCAAGCTGAAAAAGCCGATGGGTACTATTGGAGGCCGCGCAAACGAATCC    |||||
QY       137  GACCAGTTCGTATTACTCACTTTAAGATTCACTAAATACCGAGTAGAGTTAGTATGA    |||||
Db       149  GTCCGTTGCTGCTTGTCACCGGTTCAAGCGCCTCGGCAAAAGACCCGCGGTCGATTGC    |||||
QY       197  AGAGCCCATTTGACACTAGAATAATGATTCATACATATTCACTATTTCATGATACCTACAG    |||||
Db       209  CCCTGCGCTGCGGATTTGAATGATCCATCACTACTCTTTGATCCATGATATTTGGCGA    |||||
QY       257  CGATGCGATTAATGATGATTTATCGACGAGAAAATTAAACAATCATATTAAGTATATGAGT    |||||
Db       269  GCATTGGACAAAGATGATTTGGCGCGCGCACGCCAACAAACATTAAGTGTTCGCGCAGG    |||||
QY       317  GGA CTGCGATTTATGACAGGTGATGCTTTATTAAC TTAAGCATTTGAAC TTATTTCC-----
Db       329  CGATGGCCATCTTGGCGGGGAGACGGGTGTGTACGTAACGCGTTCAATGATGACCGAAA    |||||
QY       372  -AAGTGTATGATTAATTAATCAATGAAGTAAAAATTAAGTTCTACACGCTGTCAATAG    |||||
Db       389  TCACGATGAGCCGATCCCTCCTTCCTGCGGCTTCGCTCATCGAACGCTGCGCGAAG    |||||
QY       431  CAAGTGGTCACTGTGSAATGTCGCGCGTCAAAATGTTAGATGTCGAAAGCGAGGCCAAC    |||||
Db       449  CGCGCGGCTCGGAAGGATGTGTGCGCGTCAGCGACCGGATATGAGAGAGAGGGA AAAA    |||||
QY       491  CAATTGATCTTTGAACTTTTGAAATGATACACAAAACAAAACAGAGACATTATTAATT    |||||
Db       509  CGGTACGCTTTGGAGCTCGAATACATTTCACTGGCATTA AAACGGGAAAATGCTGCAT    |||||
QY       551  TTCGGTTATGAGTGCACGATATGCTAATGTGATGATGATACAACTTAAGAACAATTAG    |||||
Db       569  ACAGCGTGACGCGCGCGCTTGATGCGGCGCTGAATGCCGCGCAACCGCGAGGCTTG    |||||
QY       611  AAGATTATAGTTATCACTTTAGGATGATGTCACAGTTAAAGATGATTATTAAGTCTCT    |||||
Db       629  ACGAATTCGCGCCCCATCTAAGGCTTGCTTTCAAAATTCGGATGATATTTCTCGATATTG    |||||
QY       671  ATGATGATGAAGCAAAATTAGTAAAAAAAGTGGCGAGCGATCTTGAAAAATTAATAAGTA    |||||
Db       689  AAGGGGCAAGAAAATAATCGGGAAGCCGCTGGCGAGGAGCAAAAGCAACAAAGGA    |||||
QY       731  CGTACGTGACTTTATTAGGAAAAGATGGCGCAGAAAGATPAATGCTTATCATGAGACG    |||||
Db       749  CGTATCCAGCGTTGCTGCTGCTTGCGCGCGCAAGAAAAGTTGCGTTCCATATCGAGG    |||||
QY       791  CAGC    794
Db       809  CGGC    812

RESULT 5
US-08-333-321.-1
Sequence 1, Application US/08333321
Patent No. 5786192
GENERAL INFORMATION:
Applicant: Obata, Shusei
TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward W. Greason, Esq.
STREET: 1 Broadway
CITY: New York
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: NO.5786192epad, Windows 3.1
CURRENT APPLICATION DATA:
```

```

APPLICATION NUMBER: US/08/333,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/953,424
FILING DATE: 29-SEP-1992
APPLICATION NUMBER: JP 3-253788
FILING DATE: 01-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Greason, Edward W.
REGISTRATION NUMBER: 18,918
REFERENCE/DOCKET NUMBER: 077670/00310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-333-321-1

Query Match      18.1%; Score 155.6; DB 1; Length 893;
Best Local Similarity 50.9%; Pred. No. 5e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1

Oy      17  TGAATTAATTATAGATGACATATATGAAATTAATCGGTTGCGATAAATAATAGTAA 76
Db      29  TCAACGAGCAAAACAGCGGTGGAAACAGCGCTCTCCGTTATATAGCGCTTAAG 88
Oy      77  TGCATCTACGACTGAGAGAAAGTATGTTGTTATTCATTAATAGCTGAGATAAACCATCC 136
Db      89  GCGCGCGAGACTGAAAAGCGCATGGCTACTATTGAGCGCGCGCAACGATCC 148
Oy     137  GACCAATTCTGTTATTACTCACTTAGTTAGTTACTTAATAACGAGTATGATTAAGTATGA 196
Db     149  GTCCGTTGCTCTTCTGTGCCACCGTTCGGCGCTCGCAAAACCGCGCGTCCGATTGC 208
Oy     197  AGACGCGAATGCACTGAATGATTCATCATATTCACTTATCATGATGACCTAACAG 256
Db     209  CCGTCGCTGCGCAATGAATGATCCATACGTACTCTTTGATTCATGATGATTTGCCA 268
Oy     257  CGATGATATATGATGATTAATGACGAGAGAAATTAACAATCATTAAGTATGATGAGT 316
Db     269  GCATGACAAAGATATTTGGCGCGCGCAACCGACGACATTAAGTATTTCCGCGAGG 328
Oy     317  GGACTCGATATATGACAGTATGCTTTATTACTAAACATTTGAATTTTC---- 371
Db     329  CGATGCGCATCTTGCGCGGGAGCGGATGTTGACGCTGATCAATTTGATCACCGAA 388
Oy     372  -AATGATGATGATTAATCTGATGAAGTAAATAAAGTTCTAACAGCGCTGCAATAG 430
Db     389  TCGACGATGACGCAATCCCTCTTCCTCCGCTCGGCTCGGCTCATGCAAGCGCTGGAAAG 448
Oy     431  CAAATGCGATGTTGGAATGCGCGCGCTCAAAATGTTAGATATGCAAGCGAGCGCAAC 490
Db     449  CCGCGCGTCCGAAAGGATGTCGCGCGTACAGCGACCGCATATGAGAGAGGGGAAA 508
Oy     491  CAATGATCTTGAAAACCTTGAAATGATACAAAAAAGAGAGCATTTATTAACCTT 550
Db     509  CGCTGAGCCTTTCGAGGCTCGAATACATTCATCGGCTATAAAACGGGAAAAATGTCGAAT 568
Oy     551  TTGCGGTTATAGATGACAGATATCGCTAATGTGATGATACAACTAAAGAACTTTG 610
Db     569  ACAGGTCACAGCGCGCCCTTGATCGCGCGGCTGATGCGCGGAAACGCGGAGCTTG 628
Oy     611  AAAGTTATGATTAATTTAGGATGATGTTCCAGATTAAGATGATTTATTAAGCTGCT 670
Db     629  ACGAATTCGCGCCCATCTAGGCTTGCCTTTCAATTCGCGATGATATTTCTGATTTG 688

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QY 671 ATGTGATGAGCAAAAGTTAGTAAAGTGGACGATCTTGAATAATTAAGTA 730
Db 689 AAGGGGAGAAAAGAAAATCGGACGCGGTCCGACGACCAAGCAACAAAGCGA 748
QY 731 CGTACGTGATTTATTAGGAAAAGATGGCGACGAAGTAAATGACTTATCATAGAGC 790
Db 749 CGTATCCAGCGTTGCTGCTGCTGCGCGCGCAAGAAAAGTTGGCGTTCATATCGAGC 808
QY 791 CAGC 794
Db 809 CGGC 812

RESULT 6
US-08-534-910B-2
Sequence 2, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOYAMA, Taneoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE: Bacillus stearothermophilus
US-08-534-910B-2

Query Match 18.1%; Score 155.6; DB 1; Length 894;
Best Local Similarity 50.9%; Pred. No. 5e-29;
Matches 399; Conservative 0; Mismatches 379; Indels 6; Gaps 1;

QY 17 TGAATAAATTATAGATGAAGTCAATATATCGTTGCGATTAATAATCAGTAA 76
Db 29 TCAACGACGAAAACAGGCGGTGAAAACAGCGCTCTCCCTTATATAGACGCTTAGAG 88

QY 77 TGATACCTAGCTAGAGAAAAGTATGTTATTCATTAATGCTGAGGTAAAGCATCC 136
Db 89 GCGCGCGAAGAGTGAAGAAAAGCGATGCGTACATCTTGAAGCGCGCGGAAAGCATCC 148
QY 137 GACCACTCTGTTATTACTCATCTTATAGANTCACTAAATACGAGTATGATTAAGTATGA 196
Db 149 GTCCGTTGCTGCTTCTGTCCACCGTTCAAGCGCTCGGCAAAAGACCGCGGTGCGATTGC 208
QY 197 AGAGCGCAATGCTAGTAAATATATTCATATTCATCTTATTCATGAGACTTACAG 256
Db 209 CCGTGCCTGCGCGATTAATATATCATATCATATCTTTGATTCATATGATTTGCGA 268
QY 257 CGATGATATATGATTAATTCAGACGAGAAAATTAACAATCATTAAGTATAGTATAGT 316
Db 269 GCATGACACATGATGATTTGCGCGCGCGGACGCGGACGCAACATTAAGTTTGGCGAGC 328
QY 317 GGACTGCGATATTAGACGATGATCTTTATTAATAAGCATTTGAATTTTC----- 371
Db 329 CGATGCGCATCTTGGCGGGGAGCGGTTGTTGACGTACGAGTTTCAATGATCATCGGAAA 388
QY 372 -AAGTATGATGATTAATGATGAAATTAATAAGTTCTACACCGCTGCAATAG 430
Db 389 TCGACGATGAGCGCATCCCTCTTCGTCGCGCTTGGCTCATCGAACGCTGCGGAAAG 448
QY 431 CAAGTGTATGTTGGAATGTCGCGCGGTCGAATGTTAGTATGCAAGGAGCGCAAC 490
Db 449 CGCGCGCTCGAGAGGATGTCGCGGTACGACCGCATATGAGAGAGGAGGAAA 508
QY 491 CAATTGATCTTGAACCTTTGGAATGATACACAAAACAAAACAGGACATTTAATT 550
Db 509 CGCTGACGCTTTCGAGCTCGAATATCATTCATCGGATTAACCGGAAAATGCTGCAAT 568
QY 551 TTGCGGTATGAGTGCAGCAGATATGCTAATGTCGATGATACATTAAGAACATTTAG 610
Db 569 ACAGCGTGCACGCGCGGCTTGTATGCGCGCGCTATGCGCGCAACCGCGGAGCTTG 628
QY 611 AAAGTATATGTTATCATCTTATGATGATGTTCCAGATTAAGTATTAATTTAGACTGCT 670
Db 629 ACGAATTCGCGCGCCCATCTAGGCTTCCCTTTCAATTCGCGATGATTTCTGATATTG 688
QY 671 ATGTGATGAGCAAAAGTTAGTAAAGTGGACGCGATCTTGAATAATTAAGTA 730
Db 689 AAGGGGAGAAAAGAAAATCGGACGCGGTCCGACGACCAAGCAACAAAGCGA 748
QY 731 CGTACGTGATTTATTAGGAAAAGATGGCGACGAAGTAAATGACTTATCATAGAGC 790
Db 749 CGTATCCAGCGTTGCTGCTGCTGCGCGCGCAAGAAAAGTTGGCGTTCATATCGAGC 808
QY 791 CAGC 794
Db 809 CGGC 812

RESULT 7
US-08-534-910B-3
Sequence 3, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOYAMA, Taneoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington


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Db                809 CCGC 812

RESULT 10
US-09-475-304-1
; Sequence 1, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keisbi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; OS-09-475-304-1

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Query Match	18.1%	Score 155.6	DB 3	Length 894
Best Local Similarity	50.9%	Pred. No. 5e-29		
Matches 399	Conservative 0	Mismatches 379	Indels 6	Gaps 1
QY	17	TGAATTAATTAATAGATGACATCAATTAATGAATTATCGGTGGATTAATAATACGTAA	76	
Db	29	TCAACGAGCAAAAAACAGCGCGGTGGAAAACAGCGCTCTCCGTTATATAGACGCTTAGAAG	88	
QY	77	TGGAATCTAGCTAGAAAAGTATGTTGTATTCATTAAAGCTGAGAGTAAACCATCC	136	
Db	89	GGCGCGGAGACTGAAAAAGCGATGCGCTACTCTAGAGCCGCGCGCAACCAATCC	148	
QY	137	GACCAGTTCGTATTAATCTACTCTTAGATTCACTAAATACGAGATGAGTTAGGTATGA	196	
Db	149	GTCGCTGTCTCTCTCTGTCCACCGTTCGGGCGCTCGGCAAAACC CGCGGTGCGATTCC	208	
QY	197	AGAGCGCAATTGCACCTAGAAAATGATTCATACATATTCATTATTCATGATGACTACAG	256	
Db	209	CCGTGCGCTCGCGCATTTGAATGATTCACATCGTACTCTTGATTCATGATGATTTGGCGA	268	
QY	257	CGATGATTAAGATGATTAATGACAGAGAAAATTAAACAATCATTAAGATATGTTGATG	316	
Db	269	GCAATGACAAAGATGATTTGCGGCGCGGCAAGCCGACAAACATAAAGTTCGCGCGAGG	328	
QY	317	GGAATCGGATTTATAGCAGGTATGCTTATTAATCTAAAGCAATTGAATTTTC-----	371	
Db	329	CGATGCGCATTTTGCGCGGGAGACGGGTCTTGACGTACGCGTTCAATTGATCACCGAAA	388	
QY	372	-AAGTATGATGATTAATCTGATGAAGTAAAAATAAAAATTTCTACACGCGCTCAATNG	430	
Db	389	TCGACGATGAGCGCATCCCTCCTTCGCTCGGCTTCGCGCTCATCGAACGCGTGGGAAAG	448	
QY	431	CAAGTGGTCAATGTTGGAATGTTTCGCGCGGTCAAAATTTAGATATGCAAGCGAAAGCCAA	490	
Db	449	CGCGCGGTTCGGAAGGATGTTGCGCGGTTCAGCGACCGGATATGGAAGAGGAGGAGAAA	508	
QY	491	CAATTGATCTTGAAACTTTGAAAATGATATACAAACAAAAACAGAGCATTAATTAACCTT	550	
Db	509	CGCTGACGCTTTCCGAGCTGAAATACATTCATCCGACATAAACCGGAGAAAATGCTGCAAT	568	
QY	551	TTGCGGTTATAGTGCAGCAGATATCGCTAAATGTCGATGATACAACTAAAGAACTTNG	610	

Db	569	ACAGCGTGACACCGGCGCCTTGATCGGCGGCGCTGATGCCCGGCAACCGGGAAGCTTG	628
Qy	611	AAAGTTATAGTTATGATTTAGGTATGATGTCCTCGAGTTAAAGATGATTTATGACCTGT	670
Db	629	ACGAATTCGCCGCCCATCTAGGCTTGCTTCAAAATTCGGAATGATTTCTGATATTG	688
Qy	671	ATGCTGATGAACAAGTTAGGTAAAAAAGTGGCAGCGATCTTGAAAAATATATAAAGTA	730
Db	689	AAAGGGCAACAATAAAAAATCGGCAAGCCGGTCGGCAGCGACCAAGCAACAACAAAGCGA	748
Qy	731	CGTACGTGAGTTATTATGGGAAAGATGGCGCAGAGAATTAATTGACTTATCATAGAGACG	790
Db	749	CGATTCACAGTTGCTGTGCTTGGCGGCGGAAGAAAGATTGGCTTCCATATCGAGG	808
Qy	791	CAGC	794
Db	809	CGGC	812

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: RESULT 11
: US-09-101-126-4
: Sequence 4, Application US/09101126
: Patent No. 6316216
: GENERAL INFORMATION:
: APPLICANT: OHTO, HIKARU
: APPLICANT: NAKANE, HIROYUKI
: APPLICANT: NISHINO, TOKUZO
: APPLICANT: OHNUMA, SHINICHI
: APPLICANT: HIROOKA, KAZUTAKE
: TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
: FILE REFERENCE: 77670/566
: CURRENT APPLICATION NUMBER: US/09/101,126
: CURRENT FILING DATE: 1999-04-27
: EARLIER APPLICATION NUMBER: PCT/JP97/03921
: EARLIER FILING DATE: 1997-10-29
: EARLIER APPLICATION NUMBER: JP 8-307506
: EARLIER FILING DATE: 1996-11-05
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 4
: LENGTH: 894
: TYPE: DNA
: ORGANISM: Bacillus stearothermophilus
: FEATURE:
: OTHER INFORMATION: 256-276 is an Asp-rich coding domain
: US-09-101-126-4

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Query Match	18.1%;	Score 155.6;	DB 4;	Length 894;
Best Local Similarity	50.9%;	Pred. No. 5e-29;		
Matches 399;	Conservative 0;	Mismatches 379;	Indels 6;	Gaps 1
QY	17	TGATTAATAATTAATGATGATCAATTAATGATTAATTCGGTTGGCATTAATAATTAATCACTAA	76	
Db	29	TCACAGACAAACAGCGCGGTGAGAAACAGCGCTCCCGTTATATAGACGCTTAGAAG	88	
QY	77	TGGATCTCAGCTAAGAAAGATATGTTGTTATTTATTTAAATGCTGGAGGTAAACGATCC	136	
Db	89	GGCGCGCGAAGCTGAAAAAGCGATGGCGTACTATTGGAGGCGCGGCGAAACGATCC	148	
QY	137	GACCAATTCGTTATTATTACTCACTTTAAGTTACATAAATACGAGTATGATGATTTAGATATGA	196	
Db	149	GTCCGTGTGCTTCTGTCACCGTTGGGGGCGCTCGCCAAAGACCCGGCGGTGGATTGC	208	
QY	197	AGAGCGCAATTCACATAGAAATGATTCATATTAATCACTTAATTCATGATGACCTACAG	256	
Db	209	CCGTGCGCTCGCGCATTTGAAATGATCCATACGTACTCTTTGATTCATGATGATTTGCCA	268	
QY	257	CGATGGATTAATGATGATTATTCAGACGAGGAAAAATTACAAATCAATAAAGTATATGTTGAGT	316	
Db	269	GCATGGACACGATATTTTGGGGGGCGGCGCAAGCGACGAAACATAAAGTTTGGCGGAGG	328	
QY	317	GGATCGCATATTAGACGATGCTTTATTAATCTAAAGCATTTGAATCTTAATTC-----	371	

QY 491 CAATTGATCTTGAACCTTTGGAAATGATACACAAAACAGAGCATTTATTAATT 550
Db 509 CGCTGACGCTTTCGGAGCTCGAATATCATTCATCGGCAATAAACCGGAAATGCTGCAAT 568
QY 551 TTGCGGTATGATGCGAGCATATCGCTATATGTCATGATACACTTAAGAACATTAG 610
Db 569 ACAGCGGTGACGCGCGGCGCTTGAATCGCGCGCTGATGCGCGCAACCGGAGCTTG 628
QY 611 AAGTTATGATTTATTTATTTAGTATGATGTCAGATTAAGATTTATTTAGACTGCT 670
Db 629 ACAGATTCGCGCGCGCTTGAATGCGCTTGAATGCGGATGATATTCCTGATATTTG 688
QY 671 ATGATGATGAGCAAGATTTAGTAAAGATGCGCGCGCTTGAATTAATTAATTAAGTA 720
Db 689 AAGGGGAGAAAGAAATGCGGAGCGGCTGCGGCGGCAACCAAGCAACAAAGCGA 748
QY 731 CGTACGTGATTTATTTAGGAAAGATGCGCGAGAGATTAATTTAGCTTATGATGAGAG 790
Db 749 CGTATCGAGCGTGTGCTGCTGCGCGCGGCAAGAAAGTTGCGCTTCATATCGAGG 808
QY 791 CAGC 794
Db 809 CGGC 812

RESULT 15

US-09-217-609A-28
Sequence 28, Application US/09217609A

Patent No. 6071733
GENERAL INFORMATION:
APPLICANT: MURAMATSU, Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tameooshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yenwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,609A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/873,235
FILING DATE: 11-Jun-1997
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENETTI, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 10235/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-09-217-609A-28

Query Match 17.5%; Score 150.6; DB 3; Length 486;
Best Local Similarity 58.4%; Pred. No. 7,2e-28;
Matches 277; Conservative 0; Mismatches 194; Indels 3; Gaps 1;
QY 121 GAGGTAAACGATCCGACGAGTCTGTTATTAATCACTTAGATTCATAATACCGAG 180
Db 1 GGTGGACAGCGCATTTAGACCATTAATGTTCTGACTACTTAAGTATGTTAGGCGCAAT 60
QY 181 TATGATTTGATGATGAAGAGCGCAATTTGCACTGAATATGATATCATTTCACTATT 240
Db 61 GCACATGACGCTTTACCATTTGGCATTTGGCTTGAATGATTAAGTATTTCTTTAATT 120
QY 241 CATGATGACCTACCAAGCATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 300
Db 121 CAGGATGACTTGGCGGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 180
QY 301 AAGATATGATGATGATGATGATGATGATTAATGATTAATGATTAATGATTAATGAT 360
Db 181 AAGCGTTTATGATGAACACAGCTATATCTGCGAGATGATGATGATGATGATGATGAT 240
QY 361 GAACCTATTTCAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 420
Db 241 CAATGCAATTTTAA--ATACGAGTTAAACGAAATTAATTAATCATTTGATTAATTTA 297
QY 421 CTGTCAATGACAAAGTGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 480
Db 298 TTAAATGATCTCTTCTGATCTTAATGATTAATGATTAATGATTAATGATTAATGAT 357
QY 481 GAAGGCAACCAATTTGATCTTTGAATTTGATTAATGATTAATGATTAATGATTAATGAT 540
Db 358 GAACATTAACATTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 417
QY 541 TTATTAATCTTTGCGGTATGATGATGATGATGATTAATGATTAATGATTAATGATTAAT 594
Db 418 TTGATTCGTGACGATTTGATGATGATGATTAATGATTAATGATTAATGATTAATGAT 471

Search completed: November 29, 2003, 15:05:34
Job time : 76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 13:30:00 ; Search time 335 Seconds

(without alignments)
8467.845 Million cell updates/sec

Title: US-09-925-637-63

Perfect score: 861

Sequence: 1 atgaggaatctaccgatgaa.....tattgaatcgttgattta 861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	861	10	US-09-925-637-63
2	861	100.0	861	14	US-10-084-205-63
3	861	100.0	1893	8	US-08-781-986A-155
4	846.6	98.3	882	9	US-09-815-242-8485
5	831.6	96.6	864	9	US-09-815-242-4184
6	413	48.0	413	9	US-09-815-242-2822
7	337	39.1	337	9	US-09-815-242-3275
8	196.8	22.9	882	9	US-09-815-242-6533
9	195	22.6	7528	10	US-09-070-927A-55
10	164	19.0	811	10	US-09-974-300-1015
11	131.4	15.3	888	9	US-09-815-242-7142
12	131.4	15.3	1830121	14	US-10-329-960-1
13	124.8	14.5	876	9	US-09-815-242-9175
14	124.2	14.4	876	9	US-09-815-242-9499
15	114.2	13.3	640681	10	US-09-790-988-1
16	102.4	11.9	900	9	US-09-815-242-5972

17	102.4	11.9	900	12	US-10-006-909-11	Sequence 11, Appl
18	102.4	11.9	5963	12	US-10-006-909-13	Sequence 13, Appl
19	98.6	11.5	891	10	US-09-934-903-13	Sequence 13, Appl
20	98.6	11.5	891	10	US-09-934-868-71	Sequence 71, Appl
21	98.6	11.5	891	11	US-09-941-947A-19	Sequence 19, Appl
22	97.8	11.4	900	9	US-09-815-242-9986	Sequence 9986, Ap
23	89.6	10.4	936	9	US-09-815-242-4260	Sequence 4260, Ap
24	89.6	10.4	969	9	US-09-815-242-8505	Sequence 8505, Ap
25	88.6	10.3	819	10	US-09-925-637-65	Sequence 65, Appl
26	88.6	10.3	819	10	US-10-084-205-65	Sequence 65, Appl
27	88.6	10.3	884	8	US-08-781-986A-185	Sequence 185, Appl
28	79.6	9.2	498	10	US-09-070-927A-509	Sequence 509, Ap
29	77.4	9.0	498	10	US-09-974-300-5453	Sequence 5453, Ap
30	76	8.8	498	10	US-09-974-300-5438	Sequence 5438, Ap
31	75.2	8.7	1268	13	US-10-108-915-17	Sequence 17, Appl
32	73.4	8.5	2000	10	US-09-887-576-115	Sequence 115, Appl
33	63.8	7.4	1470	13	US-10-108-915-25	Sequence 25, Appl
34	60.8	7.1	912	9	US-09-815-242-7285	Sequence 7285, Ap
35	60.4	7.0	1062	13	US-10-108-915-15	Sequence 15, Appl
36	60.4	7.0	1087	12	US-10-349-508-15	Sequence 15, Appl
37	60	7.0	1161	13	US-10-108-915-37	Sequence 37, Appl
38	57.4	6.7	1441	13	US-10-108-915-21	Sequence 21, Appl
39	56.6	6.6	1131	10	US-09-934-778-1	Sequence 1, Appl
40	55.6	6.5	912	11	US-09-941-947A-25	Sequence 25, Appl
41	55.6	6.5	912	12	US-10-218-118-1	Sequence 1, Appl
42	54.2	6.3	981	13	US-10-349-508-18	Sequence 18, Appl
43	50.8	5.9	993	13	US-10-108-915-23	Sequence 23, Appl
44	49.6	5.8	912	9	US-09-815-242-7450	Sequence 7450, Ap
45	48.4	5.6	888	9	US-09-815-242-7873	Sequence 7873, Ap

ALIGNMENTS

US-09-925-637-63	RESULT 1
Sequence 63, Application US/09925637	
Patent No. US2002010338A1	
GENERAL INFORMATION:	
APPLICANT: Chai	
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides	
FILE REFERENCE: PB560	
CURRENT APPLICATION NUMBER: US/09/925, 637	
PRIOR FILING DATE: 2001-08-10	
PRIOR APPLICATION NUMBER: PCT/US00/23773	
PRIOR FILING DATE: 2000-08-31	
PRIOR APPLICATION NUMBER: US 60/151, 933	
PRIOR FILING DATE: 1999-09-01	
PRIOR APPLICATION NUMBER: US 08/781, 986	
PRIOR FILING DATE: 1997-01-03	
PRIOR APPLICATION NUMBER: US 08/956, 171	
PRIOR FILING DATE: 1997-10-20	
PRIOR APPLICATION NUMBER: US 60/009, 861	
PRIOR FILING DATE: 1996-01-06	
NUMBER OF SEQ ID NOS: 74	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 63	
LENGTH: 861	
TYPE: DNA	
ORGANISM: Homo sapiens	
US-09-925-637-63	
Query Match	100.0%; Score 861, DB 10; Length 861;
Best Local Similarity	100.0%; Pred. No. 3.7e-175;
Matches 861; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1	ATGAGGAATCTCCGATGAATTAATAGTGAAGCAATTAATGAATTCGGTGGG 60
1	ATGAGGAATCTCCGATGAATTAATAGTGAAGCAATTAATGAATTCGGTGGG 60
61	ATTAATTAATCAGTATGATCTCAGCTAGAGGAAGATGTGTGATTCATTAAATGCT 120
61	ATTAATTAATCAGTATGATCTCAGCTAGAGGAAGATGTGTGATTCATTAAATGCT 120

QY 121 GGAGGTAAAGCAGCCAGGTTCTGTATTACTCTAGTTAGTTCAATTAACCGAG 180
DB 121 GGAGGTAAAGCAGCCAGGTTCTGTATTACTCTAGTTAGTTCAATTAACCGAG 180
QY 181 TATGAGTTAGGTATGAAGAGCGCAATTCAGTAAGTAATGATTCATATTCATTAT 240
DB 181 TATGAGTTAGGTATGAAGAGCGCAATTCAGTAAGTAATGATTCATATTCATTAT 240
QY 241 CATGATGACCTACGAGGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 CATGATGACCTACGAGGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AAGGTATAGGTAGTGAAGTGGGATTTAGCAGGTAGTGGTATTTAGTAAAGCAT 360
DB 301 AAGGTATAGGTAGTGAAGTGGGATTTAGCAGGTAGTGGTATTTAGTAAAGCAT 360
QY 361 GAACCTATTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAACCTATTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 CTGTCAATGACCAAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGTCAATGACCAAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAACATTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GAACATTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TTGACCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TTGACCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 AATTAAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 AATTAAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CATGAGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CATGAGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 841 TTATTAAGAAATCGTTGATTTA 861

RESULT 2

US-10-084-205-63
; Sequence 63, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi, G11
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 63
; LENGTH: 861
; TYPE: DNA

ORGANISM: Staphylococcus aureus
US-10-084-205-63

Query Match 100.0%; Score 861; DB 14; Length 861;
Best Local Similarity 100.0%; Pred. No. 3.7e-175;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGATCTACCGATGAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 60
DB 1 ATGACGATCTACCGATGAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 60
QY 61 ATTAATTAATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 61 ATTAATTAATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 121 GGAGGTAAAGCAGCCAGGTTCTGTATTACTCTAGTTAGTTCAATTAACCGAG 180
DB 121 GGAGGTAAAGCAGCCAGGTTCTGTATTACTCTAGTTAGTTCAATTAACCGAG 180
QY 181 TATGAGTTAGGTATGAAGAGCGCAATTCAGTAAGTAATGATTCATATTCATTAT 240
DB 181 TATGAGTTAGGTATGAAGAGCGCAATTCAGTAAGTAATGATTCATATTCATTAT 240
QY 241 CATGATGACCTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 CATGATGACCTACGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AAGGTATAGGTAGTGAAGTGGGATTTAGCAGGTAGTGGTATTTAGTAAAGCAT 360
DB 301 AAGGTATAGGTAGTGAAGTGGGATTTAGCAGGTAGTGGTATTTAGTAAAGCAT 360
QY 361 GAACCTATTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAACCTATTCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 CTGTCAATGACCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 CTGTCAATGACCAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GAAGCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TTATTAATCTTTGCGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAACATTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 GAACATTAGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 TTGACCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 TTGACCTGCTATGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 AATTAAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 AATTAAGTACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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DB 781 CATGAGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATTAAGAAATCGTTGATTTA 861
DB 841 TTATTAAGAAATCGTTGATTTA 861

RESULT 3

US-08-781-986A-155/c
; Sequence 155, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:

Best Local Similarity 99.0%; Pred. No. 4,66-172;
Matches 852; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ATGCGAATCTACCGATGAATTAATTAAGTAAGTCAATTAATGATTCGGTGG 60
Db 1 ATGCGAATCTACCGATGAATTAATTAAGTAAGTCAATTAATGATTCGGTGG 60
QY 61 ATAAATTAATGATTAAGTGAATGATTAAGTGAATTAAGTGAATTAAGTGA 120
Db 61 ATAAATTAATGATTAAGTGAATGATTAAGTGAATTAAGTGAATTAAGTGA 120
QY 121 GAGAGTAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
Db 121 GAGAGTAACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG 180
QY 181 TATGATTAAGTGAATGAAGGCGCAATGCTACTGAATTAAGTGAATTAAG 240
Db 181 TATGATTAAGTGAATGAAGGCGCAATGCTACTGAATTAAGTGAATTAAG 240
QY 241 CATGATGACCTACGAGGATGATGAATTAAGTGAATTAAGTGAATTAAGTGA 300
Db 241 CATGATGACCTACGAGGATGATGAATTAAGTGAATTAAGTGAATTAAGTGA 300
QY 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 301 AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 GAACTTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 GAACTTATTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 CTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
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QY 481 GAAAGCCAAACCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 540
Db 481 GAAAGCCAAACCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 540
QY 541 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 TTATTAATCTTTGGGTTATGATGATGATGATGATGATGATGATGATGATG 600
QY 601 GAACATTTAAGAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 660
Db 601 GAACATTTAAGAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 660
QY 661 TTAGACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 720
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QY 721 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 AATTAAGTACGTAAGTATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 CATGATGACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 CATGATGACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 TTATTAAGAAATCGTTGATTTA 861
Db 841 TTATTAAGAAATCGTTGATTTA 861
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RESULT 5

US-09-815-242-4184
; Sequence 4184, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel

```
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4184  
LENGTH: 864  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-815-242-4184
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Query Match 96.6%; Score 831.6; DB 9; Length 864;
Best Local Similarity 98.9%; Pred. No. 7,66-169;
Matches 837; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 ATGAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 75
QY 76 ATGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 135
Db 61 ATGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 136 CGACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 195
Db 121 CGACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 196 AAGAGCGCAATGCACTAAGAAATGATTCATATTCATATTCATATTCATAT 255
Db 181 AAGAGCGCAATGCACTAAGAAATGATTCATATTCATATTCATATTCATAT 240
QY 256 GCGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 315
Db 241 GCGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 316 TGACATGCAATTTACAGATGATGATGATGATGATGATGATGATGATGATG 375
Db 301 TGACATGCAATTTACAGATGATGATGATGATGATGATGATGATGATGATG 360
QY 376 GATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 435
Db 361 GATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 436 GGTGATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 495
Db 421 GGTGATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 496 GATCTGAACTTTGAAATGATGATGATGATGATGATGATGATGATGATGAT 555
Db 481 GATCTGAACTTTGAAATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 556 GTTATGATGACGACATATGCTAATGCTAATGCTAATGCTAATGCTAATGCTA 615
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Db	541	GTATGAGTGCACGACAGTATCGCTAATGTCAGTAGTCGAACCTAAAGAACATTGAAAGT	6000
Qy	616	TATAGTTATCATTTAGATAGAGTTCGCGATTTAAAGATGATTTATTGACTCGTATGCT	6753
Db	601	TATAGTTATCATTTAGATAGAGTTCGATTTAAAGATGATTTATTGACTCGTATGCT	6606
Qy	676	GATGAAACCAAGTTAGATGAAAAAGTGGCGACGCATCTTGAAAAATATATAAAGTACGTAC	7325
Db	661	GATGAAACCAAGTTAGATGAAAAAGTGGCGACGCATCTTGAAAAATATATAAAGTACATAC	7200
Qy	736	GTCAGTTATTTAGGAAAGATGCGCGAGAAATTAATTGACTTATCATATGAGACGGCACA	7953
Db	721	GTCAGTTATTTAGGAAAGATGCGCGAGAAATTAATTGACTTATCATATGAGACGGCACA	7800
Qy	796	GTCGATGAACTAAACGCAAAATTGATGAAACAATTCATACAAAACCTTATTGAAATCGTT	8555
Db	781	GTCGATGAACTAATGCAAAATTGATGAAACAATTCATACAAAACCTTATTGAAATCGTT	8400
Qy	856	GATTTA 861	
Db	841	GATTTA 846	

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RESULT 6
US-09-815-242-2822/c
Sequence 2822, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2822
LENGTH: 413
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-815-242-2822

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		48.0%;	Score 413;	DB 9;	Length 413;
		Best Local Similarity	100.0%;	Pred. No. 4	1e-79;
	Matches 413;	Conservative	0;	Mismatches	0;
			Indels	0;	Gaps
					0
QY	160	TTAGATTCTCTAAATACCGAGTATGAGTTAGTATGAAGCGCAATTGCCTAGAAATG	219		
Db	413	TTAGATTCTCTAAATACCGAGTATGAGTTAGTATGAAGCGCAATTGCCTAGAAATG	354		
QY	220	ATTGATATCATTCATTTTATCATATATGACCTACGAGATGATATGATATATCCA	279		

Db	353	ATTCATACATATTCACCTTATTCAATGATAGCACTACACGAGTGGATATATGATATATTCGA	294
QY	280	CGAGGAAAATTTAACAAATCATTAAGTATATGGTGAATGAGCACTGCCGATATTACGAGGTGAT	339
Db	293	CGAGGAAAATTTAACAAATCATTAAGTATATGGTGAATGAGCACTGCCGATATTACGAGGTGAT	234
QY	340	GCTTATTATACCTAAAGCATTTGMACTTATTTGCAAGTGAATGATAGATTAATCATGATGAAGTA	399
Db	233	GCTTATTATACCTAAAGCATTTGMACTTATTTGCAAGTGAATGATAGATTAATCATGATGAAGTA	174
QY	400	AAAAATAAAAGTTCTTCAACCGGTGTTCATATAGCAATGGTCAATGTTGGAAATGGTCCGGCGT	459
Db	173	AAAAATAAAAGTTCTTCAACCGGTGTTCATATAGCAATGGTCAATGTTGGAAATGGTCCGGCGT	114
QY	460	CAAAATGTTAGATATGCAAAAGCGAGAGGCCAACCAATTTGATCTTTGAAACTTTGGAAATGATA	519
Db	113	CAAAATGTTAGATATGCAAAAGCGAGAGGCCAACCAATTTGATCTTTGAAACTTTGGAAATGATA	54
QY	520	CACAAAACAAAACACGAGCATTTATTAATCTTTGGGGTATATAGATGCACACAGA	572
Db	53	CACAAAACAAAACACGAGCATTTATTAATCTTTGGGGTATATAGATGCACACAGA	1

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RESULT 7
US-09-815-242-3275/c
; Sequence 3275, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3275
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-3275

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	Query Match	39.1%;	Score 337;	DB 9;	Length 337;	
	Best Local Similarity	100.0%;	Prod. No. 7.8e-63;			
	Matches 337;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
Qy	225	TACATATTCACTTATTCATGATGACCTTACGACGATGATATGATGATTATCGACGAG	284			
Db	337	TACATATTCACTTATTCATGATGACCTTACGACGATGATATGATGATTATCGACGAG	278			
Qy	285	AAATTAACTTATATTAAGTATATGTCGATGACCTCGCATATTGACAGCTGATGCTTT	344			

APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: P9369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 7528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-070-927A-55

Query Match 22.6%; Score 195; DB 10; Length 7528;
Best Local Similarity 56.9%; Pred. No. 7.5e-32;
Matches 398; Conservative 0; Mismatches 295; Indels 6; Gaps 2;

92 AAGAAATGTTGTTATTCATTAAATGCTGAGGTAAAGCCATCCAGCTTCTGTTAT 151
6730 AAGAGCAATGCTCTACTCATACACGAGGTGCAACGATTACGCCCTATTAGTGT 6789

152 TACTCCTTAGATCTCAATAACGAGTATGA---GTTAGATGAAGAAGGCAATTG 208
6790 TAACAAAGTGGCGGCTTTCAAAAAGATGAACAACAAGCTATCAAGTGGCTGCT 6849

209 CACTAGAAATGATTCATACATATTCCTTATTCATGATGACTACACGAGTGGATATG 268
6850 CTTTAGAGATGATTCATACATATTCCTTATTCATGATGATTCATCCAGCAATGAGCATG 6909

269 ATGATTTACGACGAGAAATTAACAATCATTAAGTATGTTGAGTGGATGCTGCATAT 328
6910 ATGATTTACGCTGCGCAACCAACATTAAGTATGTTGAGTGGATGCTGCATAT 6969

329 TACAGAGTATGCTTATTAATTAAGCATTTGAACCTATTTCAAGTATGATGATTA 388
6970 TACAGAGGACGCGCTTATTAACAGGTGCTATTCAGTTGCTTTC---TTTGAATCAATTAG 7026

389 CTGATGAGTAAATTAAGTCTTACACGCGCTGCTCAATAGCAAGTGCATGTTGAA 448
7027 GCTTAAGTGAATAAGTTTACTGATGCAACACTGGCAAGCGGCGGGAATCAAGCA 7086

449 TGGTGGCGGCTCAATGTTAGATATGCAAAAGCGAAGCGCAACCAATTGATCTTGAACTT 508
7087 TGGTTCGCGCCAAATGGTATGATATGAGAGAAAGTCAAGTCACTTGAAGAGT 7146

509 TGGAAATGATACCAAAACAAAACGAGCATTTATTAACCTTTGCGGTATAGAGCAG 568
7147 TACGCGCTGTTCAAGAAAGAAACCGAGCGCTTAATGTAATTCCTTAATGCTGGGG 7206

569 CAAATATCGCTAATGCTGATGATACACTTAAGAACATTTAGAAAGTTATAGTTATCAT 628
7207 GCGTATTAGCAATCAAAAGAGAAAGTCAATGTTTACGACACAGTTTGGCGATCACT 7266

629 TAGGATGATGTTCCAGATTAAAGATGATTATTAAGCTGATGATGAAGCAAGT 688
7267 ATGGCTTGGCTTTCAAAATCGTATGATCTTAATGATGACCAAGTACAGAAAGCAGATT 7326

689 TAGGTAATAAGTGGGAGGAGCTTTGAAATAATAAAGTACGTACGTAGTTATAG 748
7327 TAGGTAATAAAGTAGGCGAGATGAACGTTGAATTAAGTACGTATCCAGCTCTTCTAG 7386

749 GGAAGATGCGCAGAGATTAATTTGACTTATCATAG 787
7387 GGAATGCTGGCGCAAAAGATCGCTTAACATCAATTAG 7425

RESULT 10
US-09-974-300-1015
Sequence 1015, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berkta, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Method for Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1015
LENGTH: 811
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1015

Query Match 19.0%; Score 164; DB 10; Length 811;
Best Local Similarity 52.9%; Pred. No. 1.5e-25;
Matches 378; Conservative 0; Mismatches 330; Indels 6; Gaps 1;

88 CTAGAAAGATGTTGTTATTCATTAAATGCTGAGGTAAAGCCATCCAGCTTCTG 147
97 CTAAAGAAATCCATGCTGATCTATTTGAACCGGGGGAACGCTGAGACCGATTTG 156

148 TTATTACTGACTTTAGATTCATTAATACGAGTATAGTATGATGAAGCGCAATT 207
157 GTTCTTGGCTTCTTATGATCGTACGAAAGAAAGCGGAAATTCAGTGGATGC 216

208 GCACTAGAAATGATTCATATTCATTTATTCATGATGACTTACGAGGATGATTAAT 267
217 GCGGTGAATATGATCATATGATTCATTAATTCATGACGACCTCCCTGTATGATGAC 276

268 GATGATTAATGACGAGGAAATTAACAATCATTAAGTATGATGATGATGATGATG 327
277 GATGATCTCAAGAGATGATGACGACCAACCAAAATTTAGCGGAGGCGGCGCAT 336

328 TTAGCAGTATGCTTATTAATTAAGCATTTGAACCTTATTTTC-----AGTGAATGAT 381
337 CTGCGGGAAGCGCTTATTAACGAAAGCTTCAAAATGATCACTTCAATATGCTTCT 396

382 AGATTAATGATGATGATTAATAAATTAAGTCTTACACGCGCTGCAATGACAGTGCAT 441
397 GATGATCCGCTGAAGAGCGCATACAGATCGTGAACGATCAATTCGCGAGCGGCGCC 456

442 GTTGAATGATGCGCGCTCAATGTTAGATGATGCAAGGAGGCGCAACCAATGATCT 501
457 GAAGGATGATGCGCGCTCAATGTTAGATGATGCAAGGAGGCGCAACCAATGATCT 516

502 GAAACTTTGAAATGATTAACAAACAAAACGAGCATTTATTAATTTTGGGCTTATG 561
517 GATGAATCAGAGGATTCACAGAGAAACCGCTTAATCTCTGAGCTTCAAGCTCAT 576

562 AGTGACGAGATATGCTATGATGATGATTAACCTTAAGAACATTTAGAAAGTATAGT 621
577 GCGGAGCGCATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATG 636

622 TATCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681
637 CATCATATGCGATCGCTTTTCAATGATGATGATGATGATGATGATGATGATGATG 696

682 GCAAGTATGATTAATAAAGTGGGAGCGATCTTGAATAATTAATTAAGTACGTAGAT 741
697 GATTAATGCGCAAGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 756

Qy 742 TTATTAGGAAAGATGGCGAGAAATTAATTGACTTATCATAGAGCGAGCA 795
Db 757 CTCCTTGGCTTGAGGGCGCGAGCAAAACTTATGATGATTTGAAAAAGCA 810

RESULT 11

US-09-815-242-7142
; Sequence 7142, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyklich, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7142
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(888)
US-09-815-242-7142

Query Match 15.3%; Score 131.4; DB 9; Length 888;
Best Local Similarity 49.9%; Pred. No. 1.5e-18;
Matches 361; Conservative 0; Mismatches 356; Indels 6; Gaps 1;

Qy 100 ATGTGTTATTCATTAATGCTGGAGTAAACGATCCGACGCTTGTATTAATCACT 159
Db 109 ATGAAATACGATTAATTAATCTGGGTAAAGGAGTGGCCCTTCTTAGTTAGCAACA 168
Qy 160 TTAGATTCACAAATACGAGTATGATGATGAAGCGCAATTTGACATGAATG 219
Db 169 GGTAAATGCTTGGCGGAGAAACAACTTAATTAAGCTGCTGCGCATTAAGCC 228
Qy 220 ATTGATACATTAATCACTTATTCATGATGACCTACAGCGATGATTAATGATTAATGCA 279
Db 229 ATTACGCGATTAATCTTAATTAATCAAGATGATTAATCTGCAATGATGATGATTAATGCA 288
Qy 280 CGAGGAAATTAACAAATCATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 339
Db 289 CGTGAATCTTACTTCTTCAATTCATTAATGATGATGATGATGATGATGATGATGATGATGAT 348
Qy 340 GCTTATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 399
Db 349 GCACTGCAAAAGTTTGCATTTGAATTAATTAACCAAAACCGGATTAATTTCTACTGAACAA 408

Qy 400 AAAATAAAGTTCTACACCGCTGTCAATAGCAAGTGTGATGATGATGATGATGATGATGATGATGAT 459
Db 409 AAATGCGCTTAAATTCATTAATTTTACGCGAAGGGCTGTGTGCAAGGAATGTGTTAGGG 468
Qy 460 CAAATGTTAGATATGCAAGCGAAGCGCAACCAATGATCTTGAACCTTTGGAATGATA 519
Db 469 CAAAGTTAGATCTTATTTCTGTAGCAATTAACAGATTAATGTTAATGATTAATTAAT 528
Qy 520 CACAAAACAAAACAGAGCATTAATTAATCTTTGCGGTTATGATGATGATGATGATGATGATGATGAT 578
Db 529 CATGCTAACAAACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
Qy 579 -----TAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 633
Db 589 CCGATTTTACGCAACAAAGGTTAGAACATCTTAACCAATATGCGAAGCATTTGT 648
Qy 634 ATGATGTTCCAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
Db 649 TTAGCTTTCAGATTCAGAGATTAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Qy 694 AAAAAGTGGCGAGCGATCTTGAATTAATTAAGTACGATGATGATGATGATGATGATGATGATGAT 753
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Qy 754 GATGCGCGAGAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 813
Db 769 AGTGGTCAAAACAAAGGCGAAGATCTATATCAAGTGTGCTGATTAAGAAAA 828
Qy 814 ATT 816
Db 829 ATT 831

RESULT 12

US-10-329-960-1
; Sequence 1, Application US/10329960
; Publication No. US20030099277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragm
; FILE REFERENCE: P186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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; NAME/KEY: misc feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
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Db 437 GATATGTCGACGAGGCAAGTTTGGATATAGAGGCGACACGACCTTGCTCTGGAAG 496
Qy 506 CTTTGGAATGATACCAAAAACGAGGACATTTAACTTTGGGCTTATAGG 565
Db 497 AACTTCAGCTATTCATGCGCAATAGACTGGAAAGTTTACCTTCCCAAGCG 556
Qy 566 CAGCAGATATCGCTAATGTCGATGATACAACTTAAGATTTAGTTATC 625
Db 557 CAGCTATTATAGCTGATTTGTCACTGAAATGCGAGTGAAGCTGAAACTGTGGGTAAT 616
Qy 626 ATTAGATGATGTTCCAGATTTAAAGATTTATTAGCTGCTATGCTGATGAACAA 685
Db 617 TGATTGACTTGCTTTTCAAGTCAGAGATGATGTACTGATGTGACAGCTAGTTTGAAG 676
Qy 686 AGTTAGCTAAAAAGCGGCGACGATCTTGAATAATATAAAGTACGTACGATTTAT 745
Db 677 AATCGGTAAGACCTCAAAAGGATCTGACGCAAGAAATCACTTCTGCTTGT 736
Qy 746 TAGGGAAGATG 757
Db 737 TGGGCTTGAAG 748

RESULT 14
US-09-815-242-9499

; Sequence 9499, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Twawick, John D.
; APPLICANT: Cair, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9499
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: CDS
; LOCATION: (1)...(876)
US-09-815-242-9499

Query Match 14.4%; Score 124.2; DB 9; Length 876;
Best Local Similarity 51.6%; Pred. No. 5.3e-17;
Matches 335; Conservative 0; Mismatches 308; Indels 6; Gaps 2;
Qy 89 TAGAAGAAAGTATGTTGATTCATTAATGCTGAGAGTAAAGCATCGACGAGTTCTGT 148
Db 89 TAGAAGAAAGTATGTTGATTCATTAATGCTGAGAGTAAAGCATCGACGAGTTCTGT 148

Db 80 TAGGGAGTCTGTTCTCTATTCATTCATGCTGCTGGCAAGCGATTCGACCTTTTCTCT 139
Qy 149 TATTACTCACTTAGTTCACTAAA---TACCGAGTATGATTAAGTATGAAGGCGAA 205
Db 140 TGTTAGAAGTTCTGGAAGCTTGACAGTTACCATCAAACTGCTACGCGCAGTACCTA 199
Qy 206 TTGCACTAGAAATGATTCATACATATTCCTATTTCATGATACCTACACGCGATGA 265
Db 200 CTGCTTGAAGATGATTCATACAGGAGGATGATTCAGATGACCTTCTGCTATGATG 259
Qy 266 ATGATGATTTATGACGAGGAAAAATTAACAATCATTAAGTATATGATGATGCGA 335
Db 260 ATGACGATTTATGGAAGAGGCGGTTTAAACCAATCAACAAGAAATTCGATGAAGCCCA 319
Qy 326 TATTAGCAGTATGCTTTTATTAACTAAGCATTTGAACCTTATTTCAAGTATGAT 385
Db 320 TTTTGGCTGGAATGCTTATTTCTAGACCATATGCTTGTATGGCAGGCGAAT---T 376
Qy 386 TAACGTATGAATTAATAAATAAAGTTCTCAACGCGCTGCAATAGCAAGTGCATGTTG 445
Db 377 TGCCAAGTCAGATTAAGTGAAGTGAAGTCCCACTTATCCCTTGCTCAGGATGCTGG 436
Qy 446 GAATGCTGCGCGCTCAAAATGTTAGATATGCAAAAGCGAAGCCCAATGATCTTGAA 505
Db 437 GATGCTGCGAGGCAAGTTTGGATATGAGAGGCGAACAACGACACTTGTCTTGGAAG 496
Qy 506 CTTTGGAATGATACCAAAAACAAAACGAGCATTTAATTTGCGGCTTATAGAG 565
Db 497 AACTTCAGATTTATTCATGCGCAATAGACTGGGAAGTTACTTACCTTATCCCTTCAAGCG 556
Qy 566 CAGCAGATATCGCTAATGTCGATGATACAACTTAAGAAACATTTAGATTTATGTTATC 625
Db 557 CAGCTATTATAGCTGATTTGTCACTGAAATGCGAGTGAAGCTGAAACTGTGGGTAAT 616
Qy 626 ATTAGATGATGTTCCAGATTTAAAGATTTATTAGCTGCTATGCTATGATGAACAA 685
Db 617 TGATTGACTTGCTTTTCAAGTCAGAGATGATGATGATGATGATGATGATGATGATG 676
Qy 686 AGTTAGCTAAAAAGTGGCGACGATCTTGAATAATATAAAGTACGTA 734
Db 677 AATCGGCAAGACACTCAAAAGGATCTGACGCAAGAAATCAACCTTA 725

RESULT 15
US-09-790-988-1/c

; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 13.3%; Score 114.2; DB 10; Length 640681;
Best Local Similarity 51.4%; Pred. No. 8.7e-14;
Matches 319; Conservative 0; Mismatches 293; Indels 9; Gaps 2;
Qy 88 CTAGAAGAAAGTATGTTGATTCATTAATGCTGAGGTTAAAGCATCGACGAGTTCTG 147
Db 511231 CTTTAAAGCAATGAATATATGATTTTTCAGGATGATTAAGAAAGTGGCTTATCTTTA 511172

GenCore version 5.1.6
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3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	35.5	293	3	US-09-276-873-2
2	37	12.9	302	4	US-09-134-001C-3171
3	17	5.9	280	4	US-09-634-238-303
4	17	5.9	312	4	US-09-107-532A-6724
5	14	4.9	297	1	US-08-534-910B-7
6	14	4.9	297	1	US-08-534-910B-8
7	14	4.9	297	1	US-08-534-910B-10
8	14	4.9	297	3	US-08-886-466-2
9	14	4.9	297	3	US-09-475-304-2
10	14	4.9	297	4	US-09-101-126-3
11	14	4.9	297	4	US-09-367-528A-5
12	11	3.8	320	3	US-09-217-742-2
13	9	3.1	320	3	US-09-217-609A-6
14	9	3.1	320	3	US-08-873-235B-6
15	8	2.8	219	4	US-09-328-352-5590
16	8	2.8	285	2	US-09-187-050-12
17	8	2.8	293	2	US-08-284-465-4
18	8	2.8	293	2	US-08-284-465-3
19	8	2.8	294	2	US-08-284-465-8
20	8	2.8	297	1	US-08-534-910B-6
21	8	2.8	297	4	US-08-534-910B-9
22	8	2.8	297	4	US-09-367-528A-1
23	8	2.8	297	4	US-09-367-528A-3
24	8	2.8	333	3	US-09-187-050-2
25	8	2.8	333	3	US-09-187-050-14
26	8	2.8	333	3	US-09-187-050-16
27	8	2.8	393	3	US-09-187-050-18

28	8	2.8	393	3	US-09-187-050-20	Sequence 20, Appl
29	8	2.8	393	3	US-09-187-050-22	Sequence 22, Appl
30	8	2.8	393	3	US-09-187-050-24	Sequence 24, Appl
31	8	2.8	393	3	US-09-187-050-26	Sequence 26, Appl
32	8	2.8	393	3	US-09-187-050-27	Sequence 27, Appl
33	8	2.8	393	3	US-09-187-050-28	Sequence 28, Appl
34	8	2.8	393	3	US-09-187-050-29	Sequence 29, Appl
35	8	2.8	393	3	US-09-187-050-30	Sequence 30, Appl
36	8	2.8	393	3	US-09-187-050-31	Sequence 31, Appl
37	8	2.8	393	3	US-09-187-050-32	Sequence 32, Appl
38	8	2.8	393	3	US-09-187-050-33	Sequence 33, Appl
39	8	2.8	393	3	US-09-187-050-34	Sequence 34, Appl
40	8	2.8	401	4	US-09-252-991A-26387	Sequence 26387, A
41	7	2.4	8	3	US-09-217-609A-7	Sequence 7, Appl
42	7	2.4	8	3	US-08-873-235B-7	Sequence 7, Appl
43	7	2.4	27	1	US-08-351-365-2	Sequence 2, Appl
44	7	2.4	27	2	US-08-467-538-2	Sequence 2, Appl
45	7	2.4	211	4	US-09-252-991A-23822	Sequence 23822, A

ALIGNMENTS

```
RESULT 1
US-09-276-873-2
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Ispra
; FILE REFERENCE: GM10208
; CURRENT APPLICATION NUMBER: US/09/276,873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-276-873-2

Query Match      35.5%  Score 102; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 KLTNHRKVGEMTALLAGDALITKAPELISSDDRLTDEVKIKVLQRLSIASGHVGMVGGM 155
DB 96 KLTNHRKVGEMTALLAGDALITKAPELISSDDRLTDEVKIKVLQRLSIASGHVGMVGGM 155
QY 156 LMQSEGQPIDLETLEMHKTKTGALLTFVMSADIANVDD 197
DB 156 LMQSEGQPIDLETLEMHKTKTGALLTFVMSADIANVDD 197

RESULT 2
US-09-134-001C-3171
; Sequence 3171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3171
; LENGTH: 302
```

TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3171

Query Match 12.9%; Score 37; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ALEMHTYSLIHDDLPMANDNDYRGKLTNKKYXGEM 106
DB 79 ALEMHTYSLIHDDLPMANDNDYRGKLTNKKYXGEM 115

RESULT 3
US-09-634-238-303

Sequence 303, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Lubbers, Mark W.
APPLICANT: Dekker, James
APPLICANT: Christenson, Anna C.
APPLICANT: Holland, Rose
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: chem and methods for using them.
FILE REFERENCE: 11000.104301
CURRENT APPLICATION NUMBER: US/09/634.238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FaestSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 280
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-09-634-238-303

Query Match 5.9%; Score 17; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMANDND 91
DB 70 HTYSLIHDDLPMANDND 86

RESULT 4
US-09-107-532A-6724

Sequence 6724, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107.532A

FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 6724:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...312
SEQUENCE DESCRIPTION: SEQ ID NO: 6724:
US-09-107-532A-6724

Query Match 5.9%; Score 17; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDDLPMANDND 91
DB 93 HTYSLIHDDLPMANDND 109

RESULT 5
US-08-534-910B-7

Sequence 7, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBAI, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyozi
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534.910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.

REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
US-08-534-910B-7

Query Match
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 6
US-08-534-910B-8
Sequence 8, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus

US-08-534-910B-8

Query Match
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 7
US-08-534-910B-10
Sequence 10, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus

US-08-534-910B-10

Query Match
Best Local Similarity 4.9%; Score 14; DB 1; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 8
US-08-886-466-2

```
; Sequence 2, Application US/0886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; CURRENT FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-08-886-466-2

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 9
US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-475-304-2

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 10
US-09-101-126-3
; Sequence 3, Application US/09101126
; Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHTO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
```

```
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126
; CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
US-09-101-126-3

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 11
US-09-367-528A-5
; Sequence 5, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

Query Match
Best Local Similarity 100.0%; Score 14; DB 4; Length 297;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 EMHTYSLIHDDLP 85
DB 76 EMHTYSLIHDDLP 89

RESULT 12
US-09-275-742-2
; Sequence 2, Application US/09275742
; Patent No. 6130069
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwin Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: ispa
; FILE REFERENCE: GM10205
; CURRENT APPLICATION NUMBER: US/09/275,742
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
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LENGTH: 291
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-275-742-2

Query Match 3.8%; Score 11; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 SLIHDDLPAMD 88
DB 76 SLIHDDLPAMD 86

RESULT 13

US-09-217-609A-6
Sequence 6, Application US/09217609A
Patent No. 6071733
GENERAL INFORMATION:
APPLICANT: MURAMATSU Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: OGURA, Kyoza
APPLICANT: Koyama, Tanetoshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yenwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,609A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/873,235
FILING DATE: 11-Jun-1997
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENETTI, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 10235/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-217-609A-6

Query Match 3.1%; Score 9; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48
DB 42 AGGKRIRPV 50

RESULT 14
US-08-873-235B-6
Sequence 6, Application US/08873235B

Patent No. 6174715
GENERAL INFORMATION:
APPLICANT: MURAMATSU Masayoshi
APPLICANT: KOIKE, Ayumi
APPLICANT: OGURA, Kyoza
APPLICANT: Koyama, Tanetoshi
APPLICANT: SHIMIZU, Naoto
APPLICANT: CHO, Yenwin
TITLE OF INVENTION: Prenyl Diphosphate Synthetase Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, NW - Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,235B
FILING DATE: 11-Jun-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 154441/1996
FILING DATE: 14-Jun-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENETTI, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 10235/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-873-235B-6

Query Match 3.1%; Score 9; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 AGGKRIRPV 48
DB 42 AGGKRIRPV 50

RESULT 15
US-09-328-352-5590
Sequence 5590, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5590
LENGTH: 219
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5590

Query Match 2.8%; Score 8; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.2;

Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7	NKLIDEVN	14						
Db	31	NKLIDEVN	38						

Search completed: November 26, 2003, 15:41:12
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:40:11 : Search time 31 Seconds
(without alignments)
1707.588 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 287
Sequence: 1 MTNLPNKLIDVNNELSAVA.....ELTQIDEGNTKLLLEIVDL 287

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	287	100.0	287	10	US-09-925-637-64
2	287	100.0	287	15	US-10-084-205-64
3	197	68.6	293	9	US-09-815-242-12583
4	192	66.9	288	9	US-09-815-242-5239
5	18	6.3	293	9	US-09-815-242-10630
6	15	5.2	297	10	US-09-934-903-14
7	15	5.2	297	11	US-09-941-947A-20
8	15	5.2	297	11	US-09-941-947A-20
9	12	4.2	295	9	US-09-815-242-11239
10	12	4.2	295	9	US-09-815-242-11069
11	12	4.2	299	9	US-09-815-242-14084
12	11	3.8	291	9	US-09-815-242-13273
13	11	3.8	291	9	US-09-815-242-13597
14	11	3.8	303	9	US-09-815-242-11382
15	11	3.8	303	9	US-09-815-242-11547

16	9	3.1	287	12	US-10-166-225A-159	Sequence 159, App
17	8	2.8	171	14	US-10-108-915-24	Sequence 24, App1
18	8	2.8	226	10	US-09-981-876-145	Sequence 145, App
19	8	2.8	226	11	US-09-148-545-145	Sequence 145, App
20	8	2.8	295	9	US-09-815-242-11971	Sequence 11971, A
21	8	2.8	316	14	US-10-108-915-16	Sequence 16, App1
22	8	2.8	316	14	US-10-108-915-20	Sequence 20, App1
23	8	2.8	316	14	US-10-108-915-45	Sequence 45, App1
24	8	2.8	326	14	US-10-108-915-46	Sequence 46, App1
25	8	2.8	330	11	US-09-284-330-22	Sequence 22, App1
26	8	2.8	330	12	US-10-066-188-39	Sequence 39, App1
27	8	2.8	330	12	US-10-066-203-39	Sequence 39, App1
28	8	2.8	330	12	US-10-223-082-178	Sequence 178, App
29	8	2.8	330	12	US-10-223-082-178	Sequence 178, App
30	8	2.8	330	14	US-10-066-500-39	Sequence 39, App1
31	8	2.8	330	15	US-10-002-796-39	Sequence 39, App1
32	8	2.8	330	15	US-10-066-273-39	Sequence 39, App1
33	8	2.8	330	15	US-10-066-494-39	Sequence 39, App1
34	8	2.8	330	15	US-10-066-269-39	Sequence 39, App1
35	8	2.8	330	15	US-10-066-211-39	Sequence 39, App1
36	8	2.8	330	15	US-10-066-193-39	Sequence 39, App1
37	8	2.8	330	15	US-10-223-085-178	Sequence 178, App
38	8	2.8	330	15	US-10-226-739-39	Sequence 39, App1
39	8	2.8	330	15	US-10-223-084-178	Sequence 178, App
40	8	2.8	330	15	US-10-223-088-178	Sequence 178, App
41	8	2.8	330	15	US-10-223-090-178	Sequence 178, App
42	8	2.8	330	15	US-10-223-087-178	Sequence 178, App
43	8	2.8	330	15	US-10-223-083-178	Sequence 178, App
44	8	2.8	330	15	US-10-223-089-178	Sequence 178, App
45	8	2.8	342	14	US-10-108-915-38	Sequence 38, App1

ALIGNMENTS

```
RESULT 1
US-09-925-637-64
; Sequence 64, Application US/09925637
; Patent No. US20020103338A1
; GENERAL INFORMATION:
; APPLICANT: Chai
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
; FILE REFERENCE: PB560
; CURRENT APPLICATION NUMBER: US/09/925,637
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/151,933
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 08/781,986
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-637-64
Query Match 100.0%; Score 287; DB 10; Length 287;
Best Local Similarity 100.0%; Pred. No. 5.8e-270; Indels 0; Gaps 0;
Matches 287; Conservative 0; Mismatches 0;
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```
QY 1 MTNLPNKLIDVNNELSAVINKSWVDLTQESMLYSLNAGGRIRPVLLTLTDSLNE 60
DB 1 MTNLPNKLIDVNNELSAVINKSWVDLTQESMLYSLNAGGRIRPVLLTLTDSLNE 60
QY 61 YEIGKMSALALEMIHTYSLIHDDLPMQNDPDRRGKLTNKKYGEWTALADALTKAF 120
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Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240
QY 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 2
US-10-084-205-64
Sequence 64, Application US/10084205
Publication No. US20030049648A1
GENERAL INFORMATION:
APPLICANT: Choi, Gil
TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P515P1
CURRENT APPLICATION NUMBER: US/10/084,205
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/151,933
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patent In Ver. 3.1
SEQ ID NO 64
LENGTH: 287
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-10-084-205-64

Query Match 100.0%; Score 287; DB 15; Length 287;
Best Local Similarity 100.0%; Pred. No. 5.8e-270;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTNLPNNKLIDEVNNELSLAINKSVMDTOLESMTLSLNAAGKRIKIRPVLLLTLDLSLNT 60
Db 1 MTNLPNNKLIDEVNNELSLAINKSVMDTOLESMTLSLNAAGKRIKIRPVLLLTLDLSLNT 60
QY 61 YELGMSAIALEMIHTYSLIHDDLPAVNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120
Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240
QY 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db 241 NKSTYVSLGKDGAEKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 3
US-09-815-242-12583
Sequence 12583, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12583
LENGTH: 293
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-815-242-12583

Query Match 68.6%; Score 197; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.1e-182;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTNLPNNKLIDEVNNELSLAINKSVMDTOLESMTLSLNAAGKRIKIRPVLLLTLDLSLNT 60
Db 1 MTNLPNNKLIDEVNNELSLAINKSVMDTOLESMTLSLNAAGKRIKIRPVLLLTLDLSLNT 60
QY 61 YELGMSAIALEMIHTYSLIHDDLPAVNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120
Db 61 YELGMSAIALEMIHTYSLIHDDLPAVNDYRGRKLTNKHVGEWTAIIAGDALLTKAF 120
QY 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
Db 121 ELISSDRLTDEVKIKYVLRSLASGHVGVGOMLMOSEGOPIDELTLEMHTKTGA 180
QY 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240
Db 181 LITFAVMSAADIANVDDTTKEHLESYSYHIGMVFQIDDLDCYGEBAKLGKVGSDLEN 240

RESULT 4
US-09-815-242-5239
Sequence 5239, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5239
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5239

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Query Match 66.9%; Score 192; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 7.7e-178;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 6 MNKLIENVNKLSTVINKSVMDTQLESMTLSYNAGKRIKRPVLLITLDSINTREYELGM 65
DB 1 MNKLIENVNKLSTVINKSVMDTQLESMTLSYNAGKRIKRPVLLITLDSINTREYELGM 60
QY 66 KSAIATLEMITYSLSIHDDLPMAMDNDYRRGKLTNKKYGGEMTAIILAGDALLTAFAELISS 125
DB 61 KSAIATLEMITYSLSIHDDLPMAMDNDYRRGKLTNKKYGGEMTAIILAGDALLTAFAELISS 120
QY 126 DDLRLTEVKIKVLQRLSTIASGHVGVGGOMLDMQSECPIDLTLEMIHKTGALLTFA 185
DB 121 DDLRLTEVKIKVLQRLSTIASGHVGVGGOMLDMQSECPIDLTLEMIHKTGALLTFA 180
QY 186 VMSAADIANVD 197
DB 181 VMSAADIANVD 192

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RESULT 5
US-09-815-242-10630
; Sequence 10630, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITPA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10630

```

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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10630

```

```

Query Match 6.3%; Score 18; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 71 LEMHTYSLSIHDDLPMAMD 88
DB 71 LEMHTYSLSIHDDLPMAMD 88

```

```

RESULT 6
US-09-934-903-14

```

```

; Sequence 14, Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Matheos
; APPLICANT: Odem, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Picataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: CL1646 US NA
; CURRENT APPLICATION NUMBER: US/09/934,903
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:
; OTHER INFORMATION: Amino acid sequences encoded by ORF7
US-09-934-903-14

```

```

Query Match 5.2%; Score 15; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 77 YSLIHDDLPMAMDND 91
DB 80 YSLIHDDLPMAMDND 94

```

```

RESULT 7
US-09-934-868-72
; Sequence 72, Application US/09934868
; Patent No. US20020137190A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Matheos
; APPLICANT: Odem, James M
; APPLICANT: Schenzle, Andreas J
; APPLICANT: Schenzle, Andreas J
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: CL1596 US NA
; CURRENT APPLICATION NUMBER: US/09/934,868
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 72
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:

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OTHER INFORMATION: Amino acid sequences encoded by ORF7 - ISPa
US-09-934-868-72

Query Match 5.2%; Score 15; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMNDND 91
Db 80 YSLIHDDLPMNDND 94

RESULT 8

US-09-941-947A-20
Sequence 20, Application US/09941947A
Publication No. US2003000528A1
GENERAL INFORMATION:
APPLICANT: Brzostowicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: DiCosimo, Deana J.
APPLICANT: Koffas, Matheos
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Picataggio, Steve E.
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: C11903 US NA
CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 297
TYPE: PRT
ORGANISM: Methylobionas 16a
US-09-941-947A-20

Query Match 5.2%; Score 15; DB 11; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMNDND 91
Db 80 YSLIHDDLPMNDND 94

RESULT 9

US-09-815-242-11239
Sequence 11239, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11239
LENGTH: 295
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-11239

Query Match 4.2%; Score 12; DB 9; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMND 88
Db 80 YSLIHDDLPMND 91

RESULT 10
US-09-815-242-10069
Sequence 10069, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10069
LENGTH: 299
TYPE: PRT
ORGANISM: Escherichia coli
US-09-815-242-10069

Query Match 4.2%; Score 12; DB 9; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 YSLIHDDLPMND 88
Db 79 YSLIHDDLPMND 90


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RESULT 11
US-09-815-242-14084
; Sequence 14084, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14084
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14084

Query Match          4.2%; Score 12; DB 9; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 YSLIHDLPAMD 88
Db      79 YSLIHDLPAMD 90

RESULT 12
US-09-815-242-13273
; Sequence 13273, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

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; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13273
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13273

Query Match          3.8%; Score 11; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDLPAMD 88
Db      76 SLIHDLPAMD 86

RESULT 13
US-09-815-242-13597
; Sequence 13597, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13597

Query Match          3.8%; Score 11; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 SLIHDLPAMD 88
Db      76 SLIHDLPAMD 86

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Db 76 SLIHDLPAMD 86

RESULT 14

US-09-815-242-11382
; Sequence 11382, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 1410
; SEQ ID NO 11382
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-815-242-11382

Query Match 3.8%; Score 11; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDLP 85
Db 85 HTYSLIHDLP 95

RESULT 15

US-09-815-242-11547
; Sequence 11547, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11547
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-815-242-11547

Query Match 3.8%; Score 11; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 HTYSLIHDLP 85
Db 85 HTYSLIHDLP 95

Search completed: November 26, 2003, 15:45:38
Job time : 31 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 05:24:42 ; Search time 67 Seconds

(Without alignments)
1890.701 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453

Sequence: 1 MTTLPNNKXIDEVNNELSV.....ELTQIDQFNTKHLRIYDL 287

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09925637/runtat_26112003_153612_19044/app_query.fasta_1.455
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=p2n -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09925637@cgn2_1_1_56@runtat_26112003_153612_19044 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	98.8	882	3	US-09-276-873-1
2	1015	69.9	909	4	US-09-134-001C-334
3	657	45.2	894	1	US-08-534-910B-4
4	656	45.1	894	1	US-08-534-910B-5
5	654	45.0	893	1	US-08-333-321-1
6	653	44.9	894	1	US-08-534-910B-2
7	650	44.7	894	1	US-08-534-910B-3
8	650	44.7	894	3	US-08-886-466-1
9	650	44.7	894	3	US-09-475-304-1
10	650	44.7	894	4	US-09-101-126-4
11	650	44.7	894	4	US-09-367-528A-4
12	645	44.4	894	1	US-08-534-910B-1

13	644	44.3	894	4	US-09-367-528A-2	Sequence 2, Appl1
14	551	37.9	876	3	US-09-275-742-1	Sequence 1, Appl1
15	549	37.8	10011	4	US-08-961-527-76	Sequence 76, Appl1
16	533	36.7	939	4	US-09-107-532A-3070	Sequence 3070, Ap
17	520.5	35.8	885	3	US-09-187-050-11	Sequence 11, Appl1
18	520.5	35.8	1179	3	US-09-187-050-13	Sequence 13, Appl1
19	520.5	35.8	1179	3	US-09-187-050-15	Sequence 15, Appl1
20	520.5	35.8	1179	3	US-09-187-050-17	Sequence 17, Appl1
21	520.5	35.8	1179	3	US-09-187-050-19	Sequence 19, Appl1
22	520.5	35.8	1179	3	US-09-187-050-21	Sequence 21, Appl1
23	520.5	35.8	1179	3	US-09-187-050-23	Sequence 23, Appl1
24	520.5	35.8	1179	3	US-09-187-050-25	Sequence 25, Appl1
25	520.5	35.8	1889	3	US-09-187-050-1	Sequence 1, Appl1
26	497.5	34.2	1830121	4	US-09-557-884-1	Sequence 1, Appl1
27	497.5	34.2	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
28	480	33.0	847	4	US-09-634-238-85	Sequence 85, Appl1
29	474.5	32.7	1071	4	US-09-252-991A-10000	Sequence 10000, A
30	474.5	32.7	1206	4	US-09-252-991A-9816	Sequence 9816, Ap
31	474.5	32.7	4515	4	US-09-252-991A-10037	Sequence 10037, A
32	465.5	32.0	1131	4	US-09-420-211-1	Sequence 1, Appl1
33	442	30.4	927	4	US-09-328-352-64	Sequence 64, Appl1
34	438.5	30.2	486	3	US-09-217-609A-28	Sequence 28, Appl1
35	438.5	30.2	486	3	US-08-873-235B-28	Sequence 28, Appl1
36	438	30.1	1087	4	US-09-549-848B-15	Sequence 15, Appl1
37	438	30.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
38	405	27.9	1914	4	US-09-634-238-41	Sequence 41, Appl1
39	376.5	25.9	909	1	US-07-783-705A-7	Sequence 7, Appl1
40	376.5	25.9	6918	1	US-07-783-705A-13	Sequence 13, Appl1
41	352	24.2	536165	4	US-09-214-808-1	Sequence 1, Appl1
42	344	23.7	1284	4	US-08-858-207A-173	Sequence 173, App
43	340	23.4	1157	1	US-08-095-726-1	Sequence 1, Appl1
44	340	23.4	1157	1	US-08-095-726-3	Sequence 3, Appl1
45	340	23.4	1157	1	US-08-096-043-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1	US-09-276-873-1	Application US/09276873
US-09-276-873-1	Patent No. 6107058	
GENERAL INFORMATION:		
APPLICANT: Edwina Imogen		
APPLICANT: Gwynn, Michael		
TITLE OF INVENTION: Ispra		
FILE REFERENCE: GM10208		
CURRENT APPLICATION NUMBER: US/09/276, 873		
CURRENT FILING DATE: 1999-03-26		
NUMBER OF SEQ ID NOS: 2		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 1		
LENGTH: 882		
TYPE: DNA		
ORGANISM: Staphylococcus aureus		
US-09-276-873-1		
Alignment Scores:		
Pred. No.:	2,976-167	Length: 882
Score:	1436.00	Matches: 284
Percent Similarity:	99.30%	Conservative: 1
Best Local Similarity:	98.95%	Mismatches: 2
Query Match:	98.83%	Indels: 0
DB:	3	Gaps: 0
US-09-925-637-64 (1-287) x US-09-276-873-1 (1-882)		
QY	1	MetThAsnLeuProwMetAsnLysLeuIlLeAsGluValAsnAnGluLeuSerValAla 20
DB	1	ATACCAATCTACCGAGTAATTAATTAAGAGAGAGTCAATATTAATTAATTCGTTGCG 60
QY	21	IlleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTyriserLeuAsnAla 40
DB	61	ATTAATTAATTCAGTATGATGATCTCAGCTAGAGAAAGACATGTTGTTATTCATTAATGCT 120

US-08-534-910B-4
Sequence 4, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOTAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534, 910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toftenefti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)428-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-4
Alignment Scores:
Pred. No.: 1.85e-71 Length: 894
Score: 657.00 Matches: 133
Percent Similarity: 68.10% Conservative: 57
Best Local Similarity: 47.67% Mismatches: 83
Query Match: 45.22% Indels: 6
Gaps: 2
US-09-925-637-64 (1-287) x US-08-534-910B-4 (1-894)
QY 1 MetThrasnleuPromeLanlySleuIlleAspGluValasnaenGluLeuSerValAla 20
DB 1 ATGGCGAGCTTTCAGTTGAACGATTCTCAACGACGAAACAGCGCGTGAACGCG 60
QY 21 IleAsnlySerValMet-----AspThrGlnLeuGluGluSerMetLeuTyr 36
DB 61 CTCCTCCGTTATATAGAGCCGCTTAGAAGCGCCGCGAGCTGAAAAAGCGATGCGCTAC 120
QY 37 SerLeuasnAlaGlyGlyLysArgIleArgProValLeuLeuLeuLeuThrLeuAspSer 56
DB 121 TCATTGGAGCGCGCGGCAACGATCCGTCGTCGCTGCTGTCACCGTTGCGGCG 180

QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleIleThr 76
DB 181 CTCGCAAGACCGCGCGCGATTCGCCGTCGCGCGATTCGATTCGATTCGATTCG 240
QY 77 TyrSerLeuIleIleAspAspLeuProAlaMetAspAspAspTyrArgArgIlyLys 96
DB 241 CACTCTTATCATGATGATTTGCGGACATGACGACGATGATTTGCGGCGCGCAAG 300
QY 97 LeuThrAsnIleIleValIleTyrGlyGluTyrPheAlaIleLeuAlaIleLeu 116
DB 301 CCACGACCAACCAATGATGTCGCGGAGCGGATGCGCATCTTGCGGCGGATGTTG 360
QY 117 ThrValAlaPheGluLeuLeuSer-----SerAspAspArgLeuThrAspGluValIly 134
DB 361 ACCTACGCTTTCATGATGATTCACCGAAATCGACGATGACGATCCCTCTTCGCGG 420
QY 135 IleValleuGlnArgLeuSerIleAlaSerGlyIleValIleValIleGlyGln 154
DB 421 CTCGCGCTCATCGAAGCGCTGCGAAGCGCGCGCTCCGGAAGGATGTCGCGGTCAG 480
QY 155 MetLeuAspMetGlnSerGluGlnProIleAspLeuGluThrLeuGluMetIleIle 174
DB 481 GCAGCGCATATGAGAGAGAGGAGAAACGCTGACGCTTCGAGCTCGAATTCATTC 540
QY 175 LysThrLysThrGlyValAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAla 194
DB 541 CGCATTAACCGCGGAAATGCTGCAATACAGGCTCAGCGCGCGCTTCGATGCGCGC 600
QY 195 ValAspAspThrThrLysGluIleLeuGluSerTyrSerTyrIleLeuGlyMetMetPhe 214
DB 601 GGTGATGCGCGGCAACGCGGAGCTTGACGATTCGCGCGCATTCGATTCGCGCTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234
DB 661 CAATTCGCGATGATATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 720
QY 235 GlySerAspLeuGluLeuAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
DB 721 GCGAGCGACCAACGACCAACGACGATTCGACGCTTCGCTGCTGCTGCGCGCGC 780
QY 255 GluAspLysLeuThrTyrIleArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
DB 781 AAGGAAAGTTGACGTTTCATTCGAGGCGCGGCGCATTTACGAAACGCGCAG 837
RESULT 4
US-08-534-910B-5
Sequence 5, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOTAMA, Tanetoshi
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534, 910B

FILING DATE: 28-SEP-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-25253
 FILING DATE: 14-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Toffenetti, Judith L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 77670/398
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-1776
 TELEFAX: (202) 429-0796
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus stearothermophilus*
 US-08-534-910B-5

Alignment Scores:
 Pred. No.: 2,45e-71 Length: 894
 Score: 656.00 Matches: 133
 Percent Similarity: 67.38% Conservative: 55
 Best Local Similarity: 47.67% Mismatches: 85
 Query Match: 45.15% Indels: 6
 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-5 (1-894)

Qy 1 MetThrAnLeuPROMetAsnLysLeuLLeaSpGLuLaAnaEnGLuLeuSerValAla 20
 Db 1 ATGGCGAGCTTTCAGTTGAAACAGTTCTCAACGAGCAAAAGCGGCGGAAACACGC 60
 Qy 21 ILeaNLysSerValMet-----AspThrGLuLeuGLuGLuSerMetLeuTyr 36
 Db 61 CTCCTCCGTTATATAGACCGCTTGAAAGCGCGCGCAAGCTGAAAGGCGATGCGCTAC 120
 Qy 37 SerLeuAnLaGLuGLuYsArgLLeaRProValLeuLeuLeuLeuThrLeuAspSer 56
 Db 121 TCATTGAGGCGCGCGCAACGAAATCGCTCGTTGCTGTCACCGTTCAAGCGC 180
 Qy 57 LeuAnThrGLuTyrGLuLeuGLuMetLysSerAlaLeaLeuGLuMetLysThr 76
 Db 181 CTCGCGAAAGACCGCGGCGTCCGATTCGCCCTCGCGGATGAAATGATCCATACG 240
 Qy 77 TysSerLeuLLeaHsaAspLeuProAlaMetAspAnAspAspTyrTATATGAGLYs 96
 Db 241 TACTCTTGTATCATGATGATTTGCCAGCATGACAAAGATTTGGCGCGCGCAAG 300
 Qy 97 LeuThrAnLysValTyrGLuTyrThrAlaLeuAnLaGLuAspAlaLeuLeu 116
 Db 301 CCGACGAACATAAAGTTCCGCGAGCGCATGTCCTGGCGGGGACGGTTGTTG 360
 Qy 117 ThrLysAlaPheGLuLeuLLeaSer-----SerAspAspArgLeuThrAspGLuValLys 134
 Db 361 ACGTACCGCTTCAATGATCAACGAATCGACATGACGATGCGCATCCCTCGCTCGCG 420
 Qy 135 ILeuValLeuGLuAnArgLeuSerLLeaLysArgLysValGLuMetValGLuGLn 154
 Db 421 CTTCGCTCATCGAAGCGCTGCGCAAGCGCGCTCGGAGGAGATGTCGCCGCTCAG 480
 Qy 155 MetLeuAspMetGLuSerGLuGLuInProLLeaSpLeuGLuThrLeuGLuMetLLeaHs 174
 Db 481 GCAAGCGATATGAAAGAGGAGGAAACGCTGACGCTTCGAGCTCGAATCATTCAT 540
 Qy 175 LysThrLysThrGLuAlaLeuLeuThrPheAlaValMetSerAlaLLeaPLeaLAsn 194
 Db 541 CCGCATAAACCGGGAATAATGCTGCATATACAGCGTGCACCGCGCTTATGATCGCGCGC 600

Qy 195 ValAspAspThrThrLysGLuHLeuGLuSerTyrSerTyrHsLeuGLuMetMetPhe 214
 Db 601 GCTGATCCCGCGCAACCGCGAGCTTGACGATTCGCCCATCTAGGCTTGCCTT 660
 Qy 215 GlnIleLysAspAspLeuLeuAspCysTyrGLuAspGLuAlaLysLeuGLuLysVal 234
 Db 661 CAATTGCGCATGATATTCGATATTGAAGGCGCAGAGAAAAATCCGCAAGCGCGTC 720
 Qy 235 GlySerAspLeuLLeuAnLysSerThrTyrValSerLeuLeuGLuLysAspGLuVal 254
 Db 721 GGCAGCGACCAACCAACCAAGGACGATATCCAGCTTGCTGCTGCGCGGCGC 780
 Qy 255 GluAspLysLeuThrTyrHsArgAspAlaValAspGLuLeuThrGlnIleAsp 273
 Db 781 AAGGAAAGTTGGCGTTCCATATCGAGGCGCGCGCCATTTAGGAAGCGCGAC 837

RESULT 5
 US-08-333-321-1
 Sequence 1, Application US/08333321
 Patent No. 5786192

GENERAL INFORMATION:

APPLICANT: Obata, Shusei

TITLE OF INVENTION: FARNESYL PYROPHOSPHATE SYNTHETASE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward W. Greason, Esq.

STREET: 1 Broadway

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: No. 5786192epd, windows 3.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,321

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/953,424

FILING DATE: 29-SEP-1992

APPLICATION NUMBER: JP 3-253788

FILING DATE: 01-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Greason, Edward W.

REGISTRATION NUMBER: 18,918

REFERENCE/DOCKET NUMBER: 077670/00310

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 425-7200

TELEFAX: (212) 425-5288

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 893 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: *Bacillus stearothermophilus*
 US-08-333-321-1

Alignment Scores:
 Pred. No.: 4.31e-71 Length: 893
 Score: 654.00 Matches: 133
 Percent Similarity: 67.38% Conservative: 55
 Best Local Similarity: 47.67% Mismatches: 85
 Query Match: 45.01% Indels: 6
 Gaps: 2

US-09-925-637-64 (1-287) x US-08-333-321-1 (1-893)

QY 1 MetThrAsnLeuPromeAenLysLeuLeuAspGluValAsnAsnGluLeuSerValAla 20
||| : : : : :
Db 1 ATGGCGCAGCTTTCAGTTGAAACAGTTTCTCAGACGAGAAAAACAGCGGTGGAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGluLeuGluLeuSerMetLeuTyr 36
: : : : :
Db 61 CTCCTCCGTTATATAGAGCCCTTAGAAGGCGCGGCGGAGAGCTGAAAAAGCGATGGCGTAC 120
QY 37 SerLeuAsnAlaGlyGlyArgGlyLeuArgProValLeuLeuLeuLeuThrLeuAspSer 56
||| : : : : :
Db 121 TCATTGGAGCGCGCGGCAACAGATCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
||| : : : : :
Db 181 CTCGGCAAGACCGCGCGCTGGATTCGCGTCCGCTGCGCGGATTTGAAAGATCCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
||| : : : : :
Db 241 TACTCTTGTATCATGATGATGATTCGCGACATGACACATGATTTGCGCGCGCGCAAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
||| : : : : :
Db 301 CCGACGACCAATAAAGTTTCGCGAGCGATGCGATGCGCGGCGGCGGCGGCTGTTG 360
QY 117 ThrLysAlaPheGluLeuLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
||| : : : : :
Db 361 ACCTAGCGCTTTCATTTGATCACCAGAAATGACAGATGACGCGCATCTCTCTCCGTCGCG 420
QY 135 IleLysValLeuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
||| : : : : :
Db 421 CTCGCGCTCATCAACGCGTGGCGAAAGCGCGCGCTCGGAGAGATGTCGCGCGTCA 480
QY 155 MetLeuAspMetLeuSerGluGlnProIleAspLeuGluThrLeuGluMetIleHis 174
||| : : : : :
Db 481 GCAGCGCATATGAGAGAGAGGAGGAGAAACGCTGACGCTTCGAGATCGAATCATTCAT 540
QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
||| : : : : :
Db 541 CGGCATTAACCGGAGAAATGCTGCAATACAGCGTGCACCGCGCTTGTATGCGCGCGC 600
QY 195 ValAspAspThrThrLysGluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPhe 214
||| : : : : :
Db 601 GGTGATGCGCGGCAACGCGGAGCTTGACGATTCGCGCGCATCTAGCGCTTGCCTTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysVal 234
||| : : : : :
Db 661 CAATTCGCGCATATATTCGATATTGAAAGGCGGCAAGAAAAATTCGCAAGCGCGTC 720
QY 235 GlySerAspLeuGluAsnLeuLysSerThrTyrValSerLeuLeuGlyLysAspGlyAla 254
||| : : : : :
Db 721 GGCAGGACCAACGACCAACGACGATTCACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 255 GluAspLysLeuThrTyrHisArgAspAlaAlaValAspGluLeuThrGlnIleAsp 273
||| : : : : :
Db 781 AAGAAAAAGTTGCGCTTCATATCGAGCGCGCGCAGCGCATTTAGGAAAGCGCGAC 837

RESULT 6
US-08-534-910B-2
Sequence 2, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoze
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesyl-diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl-diphosphate And Gene Coding Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toifenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-2

Alignment Scores:
Pred. No.: 5,73e-71 Length: 894
Score: 653.00 Matches: 132
Percent Similarity: 67.388 Conservative: 56
Best Local Similarity: 47.314 Mismatches: 85
Query Match: 44.948 Indels: 6
DB: 1 Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-2 (1-894)

QY 1 MetThrAsnLeuPromeAenLysLeuLeuAspGluValAsnAsnGluLeuSerValAla 20
||| : : : : :
Db 1 ATGGCGCAGCTTTCAGTTGAAACAGTTTCTCAGACGAGAAAAACAGCGGTGGAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGluLeuGluLeuSerMetLeuTyr 36
: : : : :
Db 61 CTCCTCCGTTATATAGAGCCCTTAGAAGGCGCGGCGGAGAGCTGAAAAAGCGATGGCGTAC 120
QY 37 SerLeuAsnAlaGlyGlyArgGlyLeuArgProValLeuLeuLeuThrLeuAspSer 56
||| : : : : :
Db 121 TCATTGGAGCGCGCGGCAACAGATCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 57 LeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThr 76
||| : : : : :
Db 181 CTCGGCAAGACCGCGCGCTGGATTCGCGTCCGCTGCGCGGATTTGAAAGATCCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
||| : : : : :
Db 241 TACTCTTGTATCATGATGATGATTCGCGACATGACACATGATTTGCGCGCGCGCAAG 300
QY 97 LeuThrAsnHisLysValTyrGlyGluTyrThrAlaIleLeuAlaGlyAspAlaLeuLeu 116
||| : : : : :
Db 301 CCGACGACCAATAAAGTTTCGCGAGCGATGCGATGCGCGGCGGCGGCTGTTG 360
QY 117 ThrLysAlaPheGluLeuLeuSer-----SerAspAspArgLeuThrAspGluValLys 134
||| : : : : :
Db 361 ACCTAGCGCTTTCATTTGATCACCAGAAATGACAGATGACGCGCATCTCTCTCCGTCGCG 420

QY 135 ILeYValleuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
Db 421 CTTGGGCTCATCGAACGGCTGCGAAGCGCGCTCGAAGGAGATGGTCCGGCTAG 480
QY 155 MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
Db 481 GCAGCCCATATGGAAGAGAGGAGAAACGCTGACGCTTCGAGCTCGAATCATTCAT 540
QY 175 LysThrThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
Db 541 CGGATTAACCGGAGAAATCTCATACGCTGACGCGCGCTGATCGGCGC 600
QY 195 ValAspAspThrThrLysGlnIleLeuGlnSerTySerTyHisLeuGlyMetMetPhe 214
Db 601 GCTGATCCCGGCAACGCGGAGCTTGCAGCATTCGCGCGCATTCAGGCTTGCTTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyGlyAspGlyAlaValLeuGlyLysVal 234
Db 661 CAATTCGCGATGATTTCTCGATATTGAAAGGCGCAAGAAATCGCGCACCGCTC 720
QY 235 GlySerAspLeuGlnAsnAsnLysSerThrTyValSerLeuLeuGlyLysAspGlyAla 254
Db 721 GCGACGACCAACCAACCAACGACGATTCAGCGCTTGCTTGCTTGCGCGCGC 780
QY 255 GlnAspLysLeuThrTyHisArgAspAlaAlaValAspGlnLeuThrGlnIleAsp 273
Db 781 AAGGAAAGTTGGCTTCATATCGAGCGCGCGCATTTACGGAACCGCGAC 837

RESULT 7

US-08-534-910B-3
Sequence 3, Application US/08534910B
Patent No. 5766911

GENERAL INFORMATION:

APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: Koyama, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-3

Alignment Scores:

Pred. No.:	1,34e-70	Length:	894
Score:	650.00	Matches:	132
Percent Similarity:	67.03%	Conservative:	55
Best Local Similarity:	47.31%	Mismatches:	86
Query Match:	44.74%	Indels:	6
DB:	1	Gaps:	2

US-09-925-637-64 (1-287) x US-08-534-910B-3 (1-894)

QY 1 MetThrAsnLeuProMetAsnLysLeuIleAspGluValAsnAsnGlnLeuSerValAla 20
Db 1 ATGGCGAGCTTCAGTTGAAAGTTTCTCAACGACAAACAGCGCGTGAACAGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGlnLeuGlnGlnSerMetLeuTyr 36
Db 61 CTCTCCGTTATATAGACCGCTTAGAAGGCGCGCGCAAGCTGAAAGCGATGCGCTAC 120
QY 37 SerLeuAsnAlaGlyGlyLysArgIleArgProValLeuLeuLeuThrLeuAspSer 56
Db 121 TCATTGGAGCGCGCGCGCAACCAATCCGTCCTGCTTCTGTCACCGCTTGCGGCG 180
QY 57 LeuAsnThrGlnLysGlnLeuGlnMetLysSerAlaIleAlaLeuGlnMetIleHisThr 76
Db 181 CTCGGAAGAACCGCGCGCGATGATCCGCTGCGCGCGATGAAATGATTCATACG 240
QY 77 TyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGlyLys 96
Db 241 TACTCTTGTATTCATATGATGATTTGCCAGCATGACAAACATATTTGCGCGCGCAG 300
QY 97 LeuThrAsnHisLysValTyrglyGlnLysThrAlaIleLeuAlaGlyAspAlaLeu 116
Db 301 CCGACGACCATTAAGTGTTCGCGAGCGCATGCGCATCTTGCGCGGAGCGGCTTGTG 360
QY 117 ThrLysAlaPheGlnLeuIleSer-----SerAspAspArgLeuThrAspGluValLys 134
Db 361 ACCTAGCGGTTTCATATGATCACGAATGACGATGAGGCGATCCCTTCCTCGTCCG 420
QY 135 ILeYValleuGlnArgLeuSerIleAlaSerGlyHisValGlyMetValGlyGln 154
Db 421 CTTGGCTCATCGAACGGCTGCGAAGCGCGCTCGGAAAGGATGCGCGCGCTAG 480
QY 155 MetLeuAspMetGlnSerGlyGlnProIleAspLeuGlnThrLeuGlnMetIleHis 174
Db 481 GCAGCCGATATGGAAGAGAGGAGAAACGCTACGCTTCGAGCTCGAATCATTCAT 540
QY 175 LysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsn 194
Db 541 CGGATTAACCGGAGAAATCTCATACGCTGACGCGCGCTGATCGGCGC 600
QY 195 ValAspAspThrThrLysGlnIleLeuGlnSerTySerTyHisLeuGlyMetMetPhe 214
Db 601 GCTGATCCCGGCAACGCGGAGCTTGCAGCATTCGCGCGCATTCAGGCTTGCTTT 660
QY 215 GlnIleLysAspAspLeuLeuAspCysTyGlyAspGlyAlaValLeuGlyLysVal 234
Db 661 CAATTCGCGATGATTTCTCGATATTGAAAGGCGCAAGAAATCGCGCACCGCTC 720
QY 235 GlySerAspLeuGlnAsnAsnLysSerThrTyValSerLeuLeuGlyLysAspGlyAla 254
Db 721 GCGACGACCAACCAACCAACGACGATTCAGCGCTTGCTTGCTTGCGCGCGC 780
QY 255 GlnAspLysLeuThrTyHisArgAspAlaAlaValAspGlnLeuThrGlnIleAsp 273
Db 781 AAGGAAAGTTGGCTTCATATCGAGCGCGCGCATTTACGGAACCGCGAC 837


```

RESULT 8
US-08-886-466-1
; Sequence 1, Application US/08886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; EARLIER FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-08-886-466-1

Alignment Scores:
Pred. No.: 1,34e-70 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 3 Gaps: 1

US-09-925-637-64 (1-287) x US-08-886-466-1 (1-894)
QY 6 MetAsnLysLeuLeuLeuLeuValAsnAsnGluLeuSerValAlaLeuLeuSerVal 25
DB 28 CTCACGACGAGAAACAGCGCGGTGAAACAGCGCTCCCGTTATATAGACCGCTTAGAA 87
QY 26 MetAspThrGlnLeuGlnLeuGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyLysArgIle 45
DB 88 GGGCCGCGGAGAGCTGAAAGAGCGGATGCGTACTGATGAGCGCGGCGAAGACGATC 147
QY 46 ArgProValLeuLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlnTyrGlnLeuGlyMet 65
DB 148 CGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 207
QY 66 LysSerAlaIleAlaLeuGlnMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85
DB 208 CCCGTCGCTGCGGATGAAATGATCATACGACTCTTGATCGATGATGATGATGATG 267
QY 86 AlaMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisLysValTyrGlnGlu 105
DB 268 AGCATGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 327
QY 106 TrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuLeuSer--- 124
DB 328 GCGATGCGCATCTTGGCGGGGAGCGGTTGTCGATGACGCTTCAATTGATCACCAGAA 367
QY 125 ---SerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnAlaGluSerIle 143
DB 388 ATGACGACATAGCGCATCTCTCCGTCGCGGCTTCGCTCATCGAACGCGTCGCGAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSerGlnGluGln 163
DB 448 GGGCGCGCTCCGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
QY 164 ProIleAspLeuGlnThrLeuGlnMetIleHisLysThrLysThrGlyAlaLeuLeuThr 183
DB 508 ACCGTAGCGCTTCCGAGCTCGAATATCATTCGCGATTAACCGGAGAAAGTGTGCAA 567

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QY 184 PheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrThrLysGluHisLeu 203
DB 568 TACAGCGTCGACCGCGCGCTTGAATCGCGGCGGTGATGCGCGCAACCGCGGACCTT 627
QY 204 GluSerTyrSerTyrHisLeuGlnMetMetPheGlnIleLysAspAspLeuAspCys 223
DB 628 GACGAATTCGCGCCCATGATGCGCTTCAATTGCGCATGATATTCGATATTC 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGlnAsnLeuSer 243
DB 688 GAGGGCGCAGAAAGAAATTCGCAAGCCGTCGAGCGACGCAAGCAACAAAGCG 747
QY 244 ThrTyrValSerLeuGlnLysAspGlyAlaGluAspLysLeuThrTyrHisArgAsp 263
DB 748 ACATATTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGCGCCGACGCCCATTTACGGAACGCCGAC 837

RESULT 9
US-09-475-304-1
; Sequence 1, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohno, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; EARLIER FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
US-09-475-304-1

Alignment Scores:
Pred. No.: 1,34e-70 Length: 894
Score: 650.00 Matches: 134
Percent Similarity: 67.78% Conservative: 49
Best Local Similarity: 49.63% Mismatches: 85
Query Match: 44.74% Indels: 2
DB: 3 Gaps: 1

US-09-925-637-64 (1-287) x US-09-475-304-1 (1-894)
QY 6 MetAsnLysLeuLeuLeuValAsnAsnGluLeuSerValAlaLeuLeuSerVal 25
DB 28 CTCACGACGAGAAACAGCGCGGTGAAACAGCGCTCCCGTTATATAGACCGCTTAGAA 87
QY 26 MetAspThrGlnLeuGlnLeuGlnSerMetLeuTyrSerLeuAsnAlaGlyGlyLysArgIle 45
DB 88 GGGCCGCGGAGAGCTGAAAGAGCGGATGCGTACTGATGAGCGCGGCGAAGACGATC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlnTyrGlnLeuGlyMet 65
DB 148 CGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 207
QY 66 LysSerAlaIleAlaLeuGlnMetIleHisThrTyrSerLeuIleHisAspAspLeuPro 85

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PRIOR APPLICATION NUMBER: JP97/346686
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 4
LENGTH: 894
TYPE: DNA
ORGANISM: Bacillus stearothermophilus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(894)
US-09-367-528A-4

Alignment Scores:
Pred. No.: 1 34e-70
Score: 650.00
Percent Similarity: 67.78%
Best Local Similarity: 49.63%
Query Match: 44.74%
Matches: 134
Conservative: 49
Mismatch: 85
Indels: 2
Gaps: 1

US-09-925-637-64 (1-287) x US-09-367-528A-4 (1-894)
QY 6 MetAsnLysLeuIleAspGluValAsnAsnGluLeuSerValAlaIleAsnLysSerVal 25
DB 28 CTCACGAGAGAAAACAGCGCGTGGAAACAGCGCTCTCCGTTATATAGCGCCTTAGAA 87
QY 26 MetAspThrGlnLeuGluGluSerMetLeuTyrSerLeuAsnAlaGlyIleValGlyIle 45
DB 88 GGGCGCGCGAGCGGAAAAGGCGATGCGTACTGATGAGCGCGCGCAACGAAAC 147
QY 46 ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlnIleValGlyIleMet 65
DB 148 CGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 207
QY 66 LysSerAlaIleAlaLeuGluMetIleAspThrTyrSerLeuIleHisAspAspLeuPro 85
DB 208 CCGCGCGCGCGCGCGATGAAATGATGATGATGATGATGATGATGATGATGATGATG 267
QY 86 AlaMetAspAspAspAspTyrArgArgGlyLysLeuThrAsnHisLysValIleGlyIle 105
DB 268 AGCATGACAAACATATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 327
QY 106 TrpThrAlaIleLeuAlaGluAspAlaLeuLeuThrLysAlaIleGluLeuIleSer 124
DB 328 GCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 387
QY 125 SerAspAspArgLeuThrAspGluValIleValIleValLeuGluIleValLeuSer 143
DB 388 ATGACAGATGAGCGCATCCCTCTCCGTCGCGCTTCATGACAGCGCTGCGGAAA 447
QY 144 AlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSerGluIleGln 163
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DB 568 TACAGCGTGCAGCGCGCGCTTATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 627
QY 204 GluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuAspCys 223
DB 628 GACGAATTCGCGCGCGCTTACGCGCTTCAATTCGCGATATATTCGATATTC 687
QY 224 TyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGluAsnLysSer 243
DB 688 GAGGCGCGAGAAAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 747
QY 244 ThrValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrThrLysArgAsp 263

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DB 748 AGTATCCAGCGTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 807
QY 264 AlaAlaValAspGluLeuThrGlnIleAsp 273
DB 808 GCGGCGCGAGCGCGCATTTACGAAACCGCGAC 837

RESULT 12
US-08-534-910B-1
Sequence 1, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBARA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyozi
APPLICANT: KOYAMA, Taneoshi
TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylidiphosphate And Gene Coding There
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetli, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0796
TELEFAX: (202) 429-1776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-1

Alignment Scores:
Pred. No.: 5.52e-70
Score: 645.00
Percent Similarity: 66.63%
Best Local Similarity: 47.97%
Query Match: 44.39%
Matches: 130
Conservative: 56
Mismatch: 79
Indels: 6
Gaps: 2

US-09-925-637-64 (1-287) x US-08-534-910B-1 (1-894)
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DB 1 ATGCGCGCGCGCTTTCGATGACGATTTCTCAACGAGCGCGCGCGCGCGCGCGCGCG 60
QY 21 IleAsnLysSerValMet-----AspThrGlnLeuGluLysSerMetLeuTyr 36

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QY 107 ThrAlaIleuAlaGlyAspAlaLeuLeuThryAlaPheGluLeuIleSerSerAsp 126
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Db 7566 ATGCCCATTTTGGCTGGAGAGGCTTATCTTACACTCATATGCTGATTTGCCAGGCA 7507
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QY 127 AspArgLeuThryAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSerGly 146
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Db 7506 GAT--TTGCCCAAGCTAAGTAAAGTGAATGACCTTGCCTTATCCCTTGCCTCAGGT 7450
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QY 147 HisValGlyMetValGlyGluMetLeuAspMetGlnSerGluGlnProIleAsp 166
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Db 7449 AGTGTGGGTATGAGCAGGGCAAGTTTGGATATGAGGGCGAACAACAGCACTGTCT 7390
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QY 167 LeuGluThryLeuGluMetIleHisLysThrySerGlyAlaLeuLeuThryPheAlaVal 186
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Db 7389 TTGGAAGAATCTTCAGACTATTCATGCCAATAGACTGGGAAGTACTAGCCTATCCCTTC 7330
|||
QY 187 MetSerAlaAlaAspIleAlaAsnValAspAspThryThrySerGluHisLeuGluSerTyr 206
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Db 7329 CAAGCGGACGCTATTATAGCTGAATGTGCACCTGAATGCAAGTGAAGCTGAAGAACTGTG 7270
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QY 207 SerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCysTyrGlyAsp 226
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Db 7269 GGTGAATTGATGACTTGTCTTTCAGTCAAGATGATGATGATGATGATGATGATGATGAT 7210
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QY 227 GluAlaLysLeuGlyLysLysValGlySerAspLeuGluAsnAsnLysSerThryVal 246
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Db 7209 TTGAGAGAAATCGCCAGACACCTCAAAAGATCTGCAGGAGAGAAAATCACTATCCT 7150
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QY 247 SerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThryHisArgAspAlaAlaVal 266
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Db 7149 GCCCTGTGGGCTTGAAGAGTCCATTGCTTGTAAACCAACCTGATCAAGCTAAT 7090
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QY 267 AspGluLeuThryGlnIleAspGluGln-----PheAsnThryHisLeuLeuGluIle 284
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QY 285 ValAsp 286
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Search completed: November 30, 2003, 07:50:01
Job time : 75 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 05:44:03 ; Search time 341 Seconds
(without alignments)
2772.950 Million cell updates/sec

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Perfect score: 1453
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues
Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bases -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.csi -LIST=45 -DOCCALIGN=200 -THR SCORE=100 -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09925637@cgn_1_1_221@runtat.26112003_153613_19096
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1453	100.0	861	10 US-09-925-637-63 Sequence 63, Appl

2	1453	100.0	861	14	US-10-084-205-63	Sequence 63, Appl
3	1453	100.0	1893	8	US-08-781-986A-155	Sequence 155, App
4	1442	99.2	882	9	US-09-815-242-8485	Sequence 8485, Ap
5	1415	97.4	864	9	US-09-815-242-4184	Sequence 4184, Ap
6	690	47.5	413	9	US-09-815-242-2822	Sequence 2822, Ap
7	635	43.7	811	10	US-09-974-300-1015	Sequence 1015, Ap
8	596	41.0	882	9	US-09-815-242-6533	Sequence 6533, Ap
9	587.5	40.4	758	10	US-09-070-927A-55	Sequence 55, Appl
10	570	39.2	876	9	US-09-815-242-3275	Sequence 3275, Ap
11	549	37.8	876	9	US-09-815-242-9499	Sequence 9499, Ap
12	547	37.6	876	9	US-09-815-242-9175	Sequence 9175, Ap
13	516.5	35.5	891	10	US-09-934-903-13	Sequence 13, Appl
14	516.5	35.5	891	10	US-09-934-868-71	Sequence 71, Appl
15	516.5	35.5	891	11	US-09-941-947A-19	Sequence 19, Appl
16	504.5	34.7	1470	13	US-10-108-915-25	Sequence 25, Appl
17	497.5	34.2	888	9	US-09-815-242-7142	Sequence 7142, Ap
18	497.5	34.2	1830121	14	US-10-329-960-1	Sequence 1, Appl
19	494.5	34.0	1441	13	US-10-108-915-21	Sequence 21, Appl
20	487.5	33.6	1268	13	US-10-108-915-17	Sequence 17, Appl
21	485.5	33.4	900	9	US-09-815-242-5972	Sequence 5972, Ap
22	485.5	33.4	900	12	US-10-006-909-11	Sequence 11, Appl
23	485.5	33.4	5963	12	US-10-006-909-13	Sequence 13, Appl
24	474.5	32.7	888	9	US-09-815-242-7873	Sequence 7873, Ap
25	473	32.6	900	9	US-09-815-242-9986	Sequence 9986, Ap
26	467	32.1	1612	12	US-10-166-225A-157	Sequence 157, App
27	465.5	32.0	1131	10	US-09-934-778-1	Sequence 1, Appl
28	438	30.1	1087	12	US-10-349-508-15	Sequence 15, Appl
29	380.5	26.2	1062	13	US-10-108-915-15	Sequence 15, Appl
30	376.5	25.9	912	11	US-09-941-947A-25	Sequence 25, Appl
31	376.5	25.9	912	12	US-10-218-118-1	Sequence 1, Appl
32	375	25.8	640681	10	US-09-790-988-1	Sequence 1, Appl
33	373.5	25.7	912	9	US-09-815-242-7285	Sequence 7285, Ap
34	372.5	25.6	912	9	US-09-815-242-7450	Sequence 7450, Ap
35	356	24.5	973	13	US-10-108-915-13	Sequence 13, Appl
36	352	24.2	536165	11	US-09-939-964-1	Sequence 1, Appl
37	332	22.8	951	14	US-10-166-037-3	Sequence 3, Appl
38	328	22.6	498	10	US-09-974-300-5453	Sequence 5453, Ap
39	328	22.6	973	13	US-10-108-915-11	Sequence 11, Appl
40	326	22.4	1128	14	US-10-156-761-140	Sequence 140, Ap
41	326	22.4	9025608	14	US-10-156-761-1	Sequence 1, Appl
42	321	21.7	498	10	US-09-974-300-5438	Sequence 5438, Ap
43	315.5	21.1	888	12	US-10-166-225A-184	Sequence 184, Ap
44	311.5	21.4	969	9	US-09-815-242-8505	Sequence 8505, Ap
45	311.5	21.4	1161	13	US-10-108-915-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-925-637-63
Sequence 63, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: Chai
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US/09/925, 637
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151, 933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781, 986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956, 171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009, 861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 63
LENGTH: 861
TYPE: DNA


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Db      601 GAACATTGAAAGTATAGTATCATTTAGTATGATGTTCCAGATTAAGAATGATTTA 660
Qy      221 LeuaspCyserTyrGlyAspGluAlaValLeuGlyLysValGlySerAspLeuGluAsn 240
Db      661 TTAGACTGCTATGATGTATGAAGCAAAAGTATGTAAGTAAAGTGGCCAGCAGATCTTGAAAT 720
Qy      241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyValAspGlyLeuThrTyr 260
Db      721 AATTAAGTACGTATCGTACGACTTTTATTGGAAAGATGGCCAGAGATTAATTGACTTAT 780
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      781 CATAGAGACGACGACAGGATGAAGTAACCAAAATGATGAACATTCATCAACAAACAC 840
Qy      281 LeuLeuGluIleValAspLeu 287
Db      841 TTATTAGAAATCGTTGATTTA 861

RESULT 3
US-08-781-986A-155/c
; Sequence 155, Application US/08781986A
; Publication No. US2003054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-155

Alignment Scores:
Pred. No.: 8.55e-163 Length: 1893
Score: 1453.00 Matches: 287
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-925-637-64 (1-287) x US-08-781-986A-155 (1-1893)
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Db      1254 AATAAATAATCAGTAATGATGATCTCGCTAGAAAGAAAGTATGTTGATTCAATTAATGCT 1195
Qy      41 GlyGlyLysArgIleArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGlu 60
Db      1194 GAGAGTAACGATCCGACAGCATGTCGTTATTACTACTTTAGATTCACTAAATACCGAG 1135
Qy      61 TyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIle 80
Db      1134 TTAGAGTTAGTATGATGAAGCCCAATTCAGTAAGAAATGATTCATCATATTCATCTTATT 1075
Qy      81 HisAspAspLeuProAlaMetAspAspAspTyrArgArgGlyLysLeuThrAsnHis 100
Db      1074 CATGATGACCTTACGACGATGATTAATGATGATTAATGACGAGAAATTAACAAATTCAT 1015
Qy      101 LysValTyrGlyGluThrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPhe 120
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Qy      121 GluLeuIleSerSerAspAspArgLeuThrAspGluValLysIleLysValLeuGlnArg 140
Db      954 GAACATTATTTCAAGTATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 895
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Db      894 CAGTCATATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 835
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Db      834 GAAAGCCAAACCAATGATCTTGAATCTTGAATGATCTTGAATGATCTTGAATGATCTTGA 775
Qy      181 LeuLeuThrPheAlaValMetSerAlaIleAspIleAlaAsnValAspAspThrLys 200
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Qy      201 GluHisLeuGluSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAspLeu 220
Db      714 GAACATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
Qy      221 LeuAspCyserTyrGlyAspGluAlaValSerLeuGlyLysValGlySerSerLeuGluAsn 240
Db      654 TTAGACTGCTATGATGATGAACCAAGTATGTAAGTAAAGTGGCCAGCATCTTGAAAT 595
Qy      241 AsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyValAspGlyLeuThrTyr 260
Db      594 AATAAAGTACGTATCGTACGACTTTTATTGGAAAGATGGCCAGAGATTAATTGACTTAT 535
Qy      261 HisArgAspAlaAlaValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHis 280
Db      534 CATAGAGACGACGACGATGATGAACCAATGATGAACCAATTCATCAATCAACAAACAC 475
Qy      281 LeuLeuGluIleValAspLeu 287
Db      474 TTATTAGAAATCGTTGATTTA 454

RESULT 4
US-09-815-242-8485
; Sequence 8485, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

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US-09-925-637-64 (1-287) X US-09-815-242-4184 (1-864)

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Qy	26	MetAspThrGlnLeuGluGluSerMetLeuTyrsSerLeuAsnAlaGlyGlyValArgIle	45
Db	61	ATGATTACTACGCTTAAGAGAAAGTATGTTGTTTCATTAAATGCGGAGATTAACGCATC	120
Qy	46	ArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrgluLeuGlyMet	65
Db	121	CGACCACTTGTATTATTAACCTTAAGATTCACCTTAATACCGAGTAAGATTAAGATGATG	180
Qy	66	LysSerAlaIleAlaLeuGluMetIleHisThrTyrsSerLeuIleHisAspAspLeuPro	85
Db	181	AAGAGCGCAATTCACCTAGAAATGATTCATACATTAATTCATTATTCATGATGACCTACA	240
Qy	86	AlaMetAspAsnAspAspTyraArgArgGlyValLeuThrAsnHisLeuValTyrglyGlu	105
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Qy	106	TyrThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeuIleSerSer	125
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Qy	126	AspAspArgLeuThrAspGluValLysIleLysValLeuGlnArgLeuSerIleAlaSer	145
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Qy	146	GlyHisValAlaGlyMetValGlyGlyGlyMetLeuAspMetGlnSerGluGlyProIle	165
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Qy	166	AspLeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAla	185
Db	481	GATCTTGAAACTTTGGAAATGATACCAAAAACAAAACGAGGACCTATTAACTTTGGC	540
Qy	186	ValMetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisLeuGluSer	205
Db	541	GTTATAGTGCGACACAAATATCGCTATATGCGATATGCAACTTAAGCAATTTGGAAGT	600
Qy	206	TyrSerTyHisLeuGlyMetMetPheGlnIleLysAspAspLeuLeuAspCysTyGly	225
Db	601	TATAGTTATCATTTAGCTATGATGATGCTTTCCGATTAAGAATGATTTATTAAGCTCTCAAGT	660
Qy	226	AspGluAlaLeuLeuGlyLysLysValGlySerAspLeuGluAsnAsnLysSerThrTyr	245
Db	661	GATGAAGCGAAGTTAGTAAAAAAAGGGCAGCATCTTGAATAATATTAATTAAGTACATC	720
Qy	246	ValSerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyHisArgAspAlaAla	265
Db	721	GTAGATTATTAAGAAAGATGCGCGAGAAAGTAAATTAATGACTTAACATTAAGACGACGA	780
Qy	266	ValAspGluLeuThrGlnIleAspGluGlnPheAsnThrLysHisLeuLeuGluIleVal	285
Db	781	GTCGATGAACATAATGCAATTAATGATGACAACTTCATACAAAACCTTAATTGAATTCGTT	840
Qy	286	AspLeu 287	
Db	841	GATTTA 846	

RESULT 6
US-09-815-242-2822/c
Sequence 2822 Application IIS/09815242

;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

Alignment Scores:

Pred. No.:	7,14e-73	length:	413
Score:	690.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	47.49%	Indels:	0
DB:	9	Gaps:	0

US-09-925-637-64 (1-287) X US-09-815-242-2822 (1-413)

QY	5	LeaAsSerLeuAsnThrGluTyrGluLeuGlyMetLysSerAlaIleAlaLeuGluMet	73
Db	413	TTTGATTCCTAAATTCGAGATGATGATTAGTAGGAAGCCGAATTGCCTGAAATG	35
QY	74	LeHisThrTyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspTyrArg	93
Db	353	ATTCAATACATATTCCTATTATTCATGATGACCTACAGGAGATGGATTAATGATTAATGCA	29
QY	94	ArgGlyLysLeuThrAsnHisLysValTyrGlyIuTrrAlaIleLeuAlaGlyAsp	111
Db	293	CGAGGAAATTAACAACATCATAAAGTAAATATGCTGATGACGCGATTTTGACAGGTGAT	23
QY	114	AlaLeuLeuThrLysAlaIleGluIleuIleSerSerAspAspArgLeuThrAspGluVal	133
Db	233	GCTTATTTACTTAAAGCATTGTAACCTTATTTCAAGTAGTAGATAGATTACATCGAAGAGTA	17
QY	134	LysIleLysValLeuGlnArgLysSerIleAlaSerGlyHisValGlyMetValGlyGly	153
Db	173	AAATATAAGTTCTTCAACAGCGCTGTCAATAGCAAGTGTCAATGTTGGAATGTCGGCGGT	11
QY	154	GlnMetLeuAspMetGlnSerGluGlyGlnProIleAspLeuGluThrLeuGluMetIle	173
Db	113	CAAAATGTGATATGCAAAAGCAAGCAACCAATATGATCTTTGAAACTTTGGAATGATA	54
QY	174	HisLysThrLysThrGlyAlaLeuLeuThrPheAlaValMetSerAlaAla	190
Db	53	CAAAAAACAAAACGAGACATTATTAATCTTTGGGTTATGAGGACGCA	3

RESULT 7

US-09-974-300-1015
; Sequence 1015, Application US/09974300
; Patent No. US2002014672A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.

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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1015
LENGTH: 811
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1015

Alignment Scores:
Pred. No.: 6,85e-66 Length: 811
Score: 635.00 Matches: 125
Percent Similarity: 73.11% Conservative: 49
Best Local Similarity: 52.52% Mismatches: 62
Query Match: 43.70% Indels: 2
DB: 10 Gaps: 1

US-09-925-637-64 (1-287) x US-09-974-300-1015 (1-811)
Qy 30 LeuGlUgUSeMeLeuTySeSerLeuAsnAlaGlyLySaArgIleArgProValLeu 49
Db 97 CTCAGGAATCCATGCTACTACTGTAACCCGGGGGAAACGGCTGAGCCGATATG 156
Qy 50 LeuLeuLeuThrLeuAspSerLeuAsnThrGlyTyrGlyLeuGlyMeLeuSerAlaIle 69
Db 157 GTTTCGCGCTTCTTCACTGCTACGAAAGACGAAGACCGGAATTCAGTCGATGC 216
Qy 70 AlaLeuGluMetIleHisThrTySerLeuIleHisAspAspLeuProAlaMetAspAsn 89
Db 217 GCGGTTGAATGATCCATACGTAATTCATTAATCATGACGACCTCCCTGTATGATGAC 276
Qy 90 AspAspTyrArgArgGlyLyLeuLeuThrAsnHisAlaValTyrGlyGlyTyrPThrAlaIle 109
Db 277 GATGACCTCGAAGAGGTAAAGCCGACAAACCAAAATTTACGGGGAGCGACGCGCAT 336
Qy 110 LeuAlaGlyAspAlaLeuLeuThrTyLeuAlaPheGluLeuIleSerSerAsp-----Asp 127
Db 337 CTCGCGGAGACGCGCTTATTAACCGAAAGCTTCAAAATGATCACTTCAATATGCTTCT 396
Qy 128 ArgLeuThrAspGluValTyrIleValLeuGlnArgLeuSerIleAlaSerGlyHis 147
Db 397 GATGTATCCGCTGAAAGCGCATCAGACTGGTGAACGAGTTCGCGAGCGGGGCC 456
Qy 148 ValGlyMetValGlyGlyGlnMetLeuAspMetLeuSerGlyGlnProIleAspLeu 167
Db 457 GAAGGCAATGCGCGCGCTGATTTGATATGAAACGGAATCAAGTCGTATCTCTT 516
Qy 168 GluThrLeuGluMetIleHisTyThrTyThrGlyAlaLeuLeuThrPheAlaValMet 187
Db 517 GATGAATGCGACGCAATCCAGGAAGAAAGCGCTAACTCTCACTTCAAGCTCAT 576
Qy 188 SerAlaIleAspIleAlaAsnValAspAspThrThrTySerGluHisLeuGluSerTySer 207
Db 577 GCGGAGACCATTCATGAGATGATCGAATAAAGATCGAAGACGCGCGAATTCAGC 636
Qy 208 TyrHisLeuGlyMetMetPheGlnIleLeuAspAspLeuLeuAspCysTyrglyAspGlu 227
Db 637 CATCATTCGCGCATCGCTTCAATCATGATCAGATACATTTTGGACCTTGAAGGCTTCGAG 696
Qy 228 AlaAlaLeuGlyLyLeuValGlySerAspLeuGluAsnValSerThrTyrglyValSer 247
Db 697 GATGAATGCGCAACGATCGATCGACGCTTCAAAACGAAAGTGAAGATTCGCGCTG 756
Qy 248 LeuLeuGlyLyAspGlyAlaGluAspLeuThrTyHisArgAspAlaAla 265

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Db 757 CTCCTTCGCTTACGCGCGCCAGCCAAACCTTGATGACATATTTGAAAAAGCA 810
RESULT 8
US-09-815-242-6533
Sequence 6533, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6533
LENGTH: 882
TYPE: DNA
ORGANISM: Enterococcus faecalis
FEATURES:
NAME/KEY: CDS
LOCATION: (1)...(882)
US-09-815-242-6533

Alignment Scores:
Pred. No.: 3.43e-61 Length: 882
Score: 596.00 Matches: 134
Percent Similarity: 65.29% Conservative: 56
Best Local Similarity: 46.05% Mismatches: 91
Query Match: 41.02% Indels: 10
DB: 9 Gaps: 5

US-09-925-637-64 (1-287) x US-09-815-242-6533 (1-882)
Qy 1 MetThrAsnLeuProMetAsn-----LysLeuIleAspGluValAsnAngluLeuSer 18
Db 1 ATAGCAATTTTGTCAACGACGCTTACCGCTTGTTGAAAGAAATCATGTCGATTTT--- 57
Qy 19 ValAlaIleAsnLysSerValMetAspThrGlnLeuGluGluSerMetLeuTySerLeu 38
Db 58 -----ATCGACAGATATACGAAATGAGCGTTTGAAAGAACAAATGCTCACTCAATA 111
Qy 39 AsnAlaGlyLyLySaArgIleArgProValLeuLeuLeuLeuThrLeuAspSerLeuAsn 58
Db 112 CACGACGATGCGCAACGATTAACCCCGCTATTGTCTTAACAACAGTGGCGGCTTTTCAA 171
Qy 59 ThrGluTyGlyLeu---GlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrg 77
Db 172 AAAGAGTGAAGAAACGACAGACTATCAATGAGTGGCTGCTTATGAGATGATTCATGAT 231
Qy 78 SerLeuIleHisAspAspLeuProAlaMetAspAsnAspTyrArgArgGlyLyLeu 97

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Qy 218 AspAspLeuLeuAspCysTrgIyAspGluAlaIyLeuGlyIySlyValIglYserAsp 237
|||
Db 7290 GAGGACTTATTATGCGACAGACGAGATTAGTAAAGTAAGCCGAGAT 7349
Qy 238 LeuGluAsnAsnIySerTrgIyValSerLeuLeuGlyIyAspGlyAlaIglYAspIyS 257
|||
Db 7350 GAAGCGTTGAATAAAGTAGATCCAGCTTCTTAGGAGTTGCGCGGAAGATGCG 7409
Qy 258 LeuThrTyr 260
|||
Db 7410 CTAAACAT 7418

RESULT 10
; US-09-815-242-3275/c
; Sequence 3275, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3275
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-3275

Alignment Scores:
Pred. No.: 1,04e-58 Length: 337
Score: 570.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.23% Indels: 0
Gaps: 0

US-09-925-637-64 (1-287) x US-09-815-242-3275 (1-337)
Qy 76 ThrTyrSerLeuIleHisAspAspLeuProAlaMetAspAsnAspAspTyrArgArgGly 95
|||
Db 336 ACATATTCATCTTATTCATGATGACCTACCGCATGATGATATGATTTCACGCGGA 277
Qy 96 LysLeuThrAsnIleIySlyValIyTrgIyGluTrpThrAlaIleLeuAlaIglYAspAlaLeu 115
|||
Db 276 AAATTAAACAATCAATAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 217
Qy 116 LeuThrLysAlaIheGluLeuIleSerSerAspAspArgLeuThrAspGluValIySlyIle 135
|||
Db 216 TTAACTAAAGCATTTGAATCTTATTTCAAGTGAATGATGATTAATCTGATGAAGTAAATAATA 157
```

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Qy 136 LysValLeuGlnArgLeuSerIleAlaSerGlyHisValIglYMetValIglYIleIleMet 155
|||
Db 156 AAGGTTCTACAGGAGGCTGCTCAATGACAGATGCTGATGATGATGATGATGATGATGATGATG 97
Qy 156 LeuAspMetGlnSerIleGluGlnProIleAspLeuGluThrLeuGluMetIleHisIySly 175
|||
Db 96 TTGATATGCAAGGCAAGGCGCAACCAATGATCTTGAAACTTGGAAATGATGATACCAAA 37
Qy 176 ThrLysThrGlyAlaLeuLeuThrPheAlaValMet 187
|||
Db 36 ACAAAAACAGAGCATTTATTAATCTTTCGCGTTATG 1

RESULT 11
; US-09-815-242-9499
; Sequence 9499, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9499
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(876)
US-09-815-242-9499

Alignment Scores:
Pred. No.: 1,35e-55 Length: 876
Score: 549.00 Matches: 121
Percent Similarity: 65.27% Conservative: 50
Best Local Similarity: 46.18% Mismatches: 87
Query Match: 37.78% Indels: 4
Gaps: 3

US-09-925-637-64 (1-287) x US-09-815-242-9499 (1-876)
Qy 28 ThrGluLeuGluIleuSerMetLeuTyrSerLeuAsnAlaIglYIySlyArgIleArgPro 47
|||
Db 73 TCTAGTTACGGAGAGCTGTTCTCTTATTCATGCTGATGATGATGATGATGATGATGATGATG 132
Qy 48 ValLeuLeuLeuLeuThrLeuAspSerLeuAsn--ThrGluTyrGluLeuGlyMetLys 66
|||
Db 133 TTCTCTTGTAGAACTTGGAAAGCTTGCAAGGTTACCATCAAACTGCTACGCGCAG 192
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QY 67 SerAlaIleuAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspLeuProAla 86
DB 193 GTAGCTACTGCTTGGAGATGATTCATACAGGAGCTTGAATCCATGACCTTCCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleValTyrGlyGluTyr 106
DB 253 ATGAGATGATGACATTTATCGAAGGGCGGTTAAACCAATCAAGAAATCGGTGAAGCT 312
QY 107 ThrAlaIleuAlaLeuAlaLeuThrLysAlaIleGluLeuIleSerSerAsp 126
DB 313 ATGGCCATTTTGGCTGAGATGCTTATTTCTTAGACCCCAATATGCTTGAATGGCGAGCA 372
QY 127 AspArgLeuThrAspGluValIleLysIleValLeuGluIleArgLeuSerIleAlaSerGly 146
DB 373 GAT---TTGCCAAGTCAGATTAAGGTGAGCTTATTCCTCACTTCCTTCAGGT 429
QY 147 HisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAsp 166
DB 430 AGCTGGGTATGGTGGCAGGCAAGTTTGGATATGAGGCGCAACACGACCTGTCT 489
QY 167 LeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
DB 490 TTGGAAAGAACTTCAGATTATTCATGCCAATAGACTGGGAAGTACTAGCTATCCCTTC 549
QY 187 MetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisIleGluSerTyr 206
DB 550 CAAGCGGACGACTTTTATGCTGAATGCTCCTGAAATGCAAGGTGAAGCTGAAGAGCTG 609
QY 207 SerTyrHisLeuGluGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
DB 610 GGTGAATTTGATTTGACTGCTTTCATGAGTCAAGATGATGATGATGATGATGATGATG 659
QY 227 GluAlaLysLeuGluGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
DB 670 TTGAGAAATCCGCAAGCAACCTCAAAAGATCTGCAGAGCAAGAAATCAACTATCC 729
QY 247 SerLeuLeuGlyLysAspGlyAlaGluAspLysLeuThrTyrHisArgAspAlaAlaVal 266
DB 730 GCGCTTTGGGCTTGGAGAGATGCTATTCCTTTGTAACCAACCTGCGATCAAGCTAAT 789
QY 267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLysHisIleLeuGluIle 284
DB 790 GAAAAATTTGAAGAAATTTGCCACAGCTTCCTTTGAAGAACAGATCGATGTAAGCTA 849
QY 285 ValAsp 286
DB 850 GTAGAA 855

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RESULT 12
US-09-815-242-9175
Sequence 9175, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9175
LENGTH: 876
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(876)
US-09-815-242-9175
Alignment Scores:
Pred. No.: 2,339-55 Length: 876
Score: 547.00 Matches: 120
Percent Similarity: 64.89% Conservative: 50
Best Local Similarity: 45.80% Mismatches: 88
Query Match: 37.65% Indels: 4
DB: 9 Gaps: 3
US-09-925-637-64 (1-287) x US-09-815-242-9175 (1-876)
QY 28 ThrGluLeuGluGluSerMetLeuTyrSerLeuAsnAlaGlyLysArgIleArgPro 47
DB 73 TCTAGTTACGGAGAGCTGCTTCTTATTCATGCTGCTGCGAAGCTATTCGGCT 112
QY 48 ValLeuLeuLeuThrLeuAspSerLeuAsnThrGluTyrGlu---LeuGlyMetLys 66
DB 133 TTCTCTTGTGAAGATTTGCAAGCTTCGACGTTGCCATCAACCTGCTCAGCGCAG 192
QY 67 SerAlaIleuAlaLeuGluMetIleHisThrTyrSerLeuIleHisAspLeuProAla 86
DB 193 GTAGCTACTGCTTGGAGATGATTCATACAGGAGCTTGAATCCATGACCTTCCTGCT 252
QY 87 MetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleValTyrGlyGluTyr 106
DB 253 ATGAGATGATGACATTTATCGAAGGGCGGTTAAACCAATCAAGAAATCGGTGAAGCT 312
QY 107 ThrAlaIleuAlaLeuAlaLeuThrLysAlaIleGluLeuIleSerSerAsp 126
DB 313 ATGGCCATTTTGGCTGAGATGCTTATTTCTTAGACCCCAATATGCTTGAATGGCGAGCA 372
QY 127 AspArgLeuThrAspGluValIleLysIleValLeuGluIleArgLeuSerIleAlaSerGly 146
DB 373 GAT---TTGCCAAGTCAGATTAAGGTGAGCTTATTCCTCACTTCCTTCAGGT 429
QY 147 HisValGlyMetValGlyGlyGlnMetLeuAspMetGlnSerGluGlnProIleAsp 166
DB 430 AGCTGGGTATGGTGGCAGGCAAGTTTGGATATGAGGCGCAACACGACCTGTCT 489
QY 167 LeuGluThrLeuGluMetIleHisLysThrLysThrGlyAlaLeuLeuThrPheAlaVal 186
DB 490 CTGGAAGAACTTCAGATTATTCATGCCAATAGACTGGGAAGTACTAGCTATCCCTTC 549
QY 187 MetSerAlaAlaAspIleAlaAsnValAspAspThrThrLysGluHisIleGluSerTyr 206
DB 550 CAAGCGGACGACTTTTATGCTGAATGCTCCTGAAATGCAAGGTGAAGCTGAAGAGCTG 609
QY 207 SerTyrHisLeuGluGlyMetMetPheGlnIleLysAspAspLeuAspCysTyrGlyAsp 226
DB 610 GGTGAATTTGATTTGACTGCTTTCATGAGTCAAGATGATGATGATGATGATGATGATG 659
QY 227 GluAlaLysLeuGluGlyLysLysValGlySerAspLeuGluAsnLysSerThrTyrVal 246
DB 670 TTGAGAAATCGGTGAAGCAACCTCAAAAGATCTGCAGGCAAGAAATCAACTATCC 729

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Oy      247 SerLeuLeuGLyLyAspLylValGluApuLyLeuThrTyrlsArgApAlaIVal 266
Db      730 GCCTTGTTCGGCCTTGGAAGATCCATTGCCTTTGTAAACCAACCCTGCATTAAGTAA 789
Oy      267 AspGluLeuThrGlnIleAspGluGln-----PheAsnThrLyshIsleuLeuGluile 284
Db      790 GAAAATAATGGAAGAATAATGCCAGACAGGTTCCCTTTGAAACAAGAAATCGATTGAAGTGA 849
Oy      285 ValAsp 286
Db      850 GTAGAA 855

RESULT 13
US-09-934-903-13
; Sequence 13, Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Kofias, Matheos
; APPLICANT: Odom, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Picataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: CL1646 US NA
; CURRENT APPLICATION NUMBER: US/09/934, 903
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229, 907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Methylobomonas 16a
; FEATURE:
; OTHER INFORMATION: ORF7
US-09-934-903-13

Alignment Scores:
Pred. NO.: 1,03e-51 Length: 891
Score: 516.50 Matches: 113
Percent Similarity: 63.75% Conservative: 47
Best Local Similarity: 45.02% Mismatches: 88
Query Match: 35.55% Indels: 3
DB: 10 Gaps: 2

US-09-925-637-64 (1-287) x US-09-934-903-13 (1-891)
Oy      23 LySserValMetAspThrGlnLeuGlnGlnSerMetLeuTySerLeuAsnAlaGlyGly 42
Db      76 GAAAAACAATACATCCCAACAAACTTGCATCGAGCATCGCTAATCCGTAATGAACGGCGGC 135
Oy      43 LysAagGlieArgProValLeuLeuLeuLeuThrLysAspSerLeuAsnThrGlnuTyrgln 62
Db      136 AAACCCACCCCGCCCTGTGTGACTTATGCGACCGCGGTGACGCTTTGGCGCTTGGCCGGAAC 195
Oy      LeuGlyMetLysSerAlaIleAlaLeuGlnMetIleHisThrTySerLeuIleHisAsp 82
Db      196 GTGCTGAGATGCCCGCGGCTTGGCGCGGTAGAAATTCATCAATGTATTCGCTGATTCAGAC 255
Oy      AspLeuProAlaMetAspAsnAspAspTYrarGargLyLysLeuThrAsnHisLysVal 102
Db      256 GATCGCGCGGCATGACACACATGATGTGCGCGCGGCAACCGACCTGTGCACAAAGGCT 315
Oy      TyrglyGluTrpThrAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeu 122
Db      316 TACGACGAGGCCACCGCCCATTTTGGCGCGCGCACGCACTCAGGCGGCTGGCTTGAAGTT 375
Oy      IleSerSerAspAspArgLeuThrAspGlu-----ValLysAlleLysValLeuGlnArg 140
Db      123 ILESERSERASPAAPARGLEUTHRASPGLU-----VALLYSALLEYSLVALLGULNARG 140

```

```
Db      376 CTGGCCAAAGACACCCTCGCATCAACCGTCATGCCCCGCCGTGCCTGAATAATGATCAGGCT
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer
          :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      436 TTGACCCGCGCCGACGGCTCTTCAAGGCAAGTGCGGCGGTCAAGCCATGATCTCGGCTCC
Qy      161 GtUGlYgInPrIleApsrLeuGluThrLeuGluMetIleHisLeuTherGlyTrGlyAla
          |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      496 GTCGGCCCGCAAATTGACCGCTCCCGGAATCTGAAAAACAATGATATCCACAAGACTGGCC
Qy      181 leuLeuThrPheAlaVal--MetSerAlaIleAsprIleAlaAspValAspAspThrThr
          |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      556 CTGATCGCGCGCACGCTCATCTGGGGGCGATTATCAAAACCGATCTGGATCTTGGCTGC
Qy      200 lyeGlUhiIsleugluseTyrrTyrlsleuglYmeMetPheGlnIleLysAspAsp
          ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      616 GCCAAGAAATGGATATCATCTATGCCAAATGATAGCGCTTGTCGTTCCAGTCCAAGAACAC
Qy      220 leuLeuAspCyrrTyrgLyaspGluAlalysleuglYlYlsValIGlYserAspLeuGlu
          ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      676 ATTCTGCACATCGAACCCGACACCGGACACTGGCGMAAGCTCAGGGCAAGACATGCAT
Qy      240 AsnAsnLysSerThrTyrlValserLeuLeuglYlysAspGlyAlagluAspLysLeuThr
          ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      736 AAGACAAACCCGACTTAACCTCGGCTATGGCGCATGGCGTGGCGCAAAACAAGGCCAG
Qy      260 TyrHisArgAspAlaAlaValAspGluLeuThr
          ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      796 GAATTGCACGAMCAMGACGCTGCAAAAGCTTAAACG
RESULT 14
US-09-934-868-71
; Sequence 71, Application US/09934868
; Patent No. US20020137190A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Mattheos
; APPLICANT: Odum, James M
; APPLICANT: Schenzle, Andreas J
; TITLE OR INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: CL1596 US NA
; CURRENT APPLICATION NUMBER: US/09/934,868
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 71
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Methylomonas 16a
; FEATURE:
; OTHER INFORMATION: ORF7 ISPA
US-09-934-868-71

Alignment Scores:
Pred. No.:      1,036-51      Length:      891
Score:         516.50        Matches:     113
Percent Similarity: 63.75%    Conservative: 47
Best Local Similarity: 45.02%   Mismatches:  88
Query Match:    35.55%       Indels:      3
Db:            10           Gaps:        2

US-09-925-637-64 (1-287) x US-09-934-868-71 (1-891)
Qy      23 LysSerValMetCysPsrGlnleuglucgluseMetLeuTyrrSerleuAsnAlaGlyGly
          :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      76 GAAAACATACCTGCACAAACCTTGATCATGACGCGCATTCCTCGATTGAAGGGGGC
Qy      43 LysArgIleArgProValleuLeuLeuLeuThrIleuAspSerleuLeuThrGluGlu
          |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      136 AAACGACACCGGCGCTTGTTGACTTATGCGACCGGTCAGGCTTGGCGCTTCCGAAAC
Qy      63 leuGlyMetLysSerAlaIleAlaleuLeuGluMetIleHisThrTyrrSerleuIleHisAsp
```



```

Db      196 GTCTGGATCGCGCGCTTCGCGGTAATTCATCATGATGATTCGATTCACAGAC 255
Qy      83 AspleuPro1aMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleVal 102
Db      256 GATCTGCGCGCCAGCAAGATGATCTGCGCGCGCAACCGAAGCTGTCAAGAGCT 315
Qy      103 TyGlyGlnThrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeu 122
Db      316 TACGACAGAGCCACCGCATTTTGCGCGGACGCACTGACAGCGCGCTTGAAAGTT 375
Qy      123 IleSerSerAspAspArgLeuThrAspGlu-----ValLysIleLysValLeuGlnArg 140
Db      376 CTGGCCACAGACCCCGCATCACCCTGATGCGCGCGCTGCGCTGAAATATGATCAGGCT 435
Qy      141 LeuSerIleLeuAspArgLysIleValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      436 TTGACCCGCGCGCGCTCTCAAGGATGTGGCGGTCAAGCCATCGATCTCGGCTCC 495
Qy      161 GluGlyGlnProIleAspLeuGlnThrLeuGluMetIleHisLysThrLysThrGlyAla 180
Db      496 GTGCGCGCGCAATTCAGCGTCCGCGAATCTGAAACATGATATCCACAGACTGGCGCC 555
Qy      181 LeuLeuThrPheAlaVal---MetSerAlaIleAspIleAlaAsnValAspAspThrThr 199
Db      556 CTGATCCGCGCGCATGCTGCGGCGATTCGCAACCCGATCTGATCTTGGCTC 615
Qy      200 LysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAsp 219
Db      616 GCCAAGAACTGTGATCATATGCGCAATGCAATGAGCTTGTCTTCCAGGTCGCAAGCGAC 675
Qy      220 LeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGlu 239
Db      676 ATTTCTGACATTCGACAGCCGACCGGACACTGGCAAGACTCAGGCGAAGACATCGAT 735
Qy      240 AsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGlnAspLysLeuThr 259
Db      736 AACGACAAACCGACCTACCTCGGCTATTGGCATGGCTGGCCCAACAAAGCCGAC 795
Qy      260 TyrHisArgAspAlaAlaValAspGluLeuThr 270
Db      796 GAATTCACGAAACAGACATCGAAGCTTAACG 828

```

RESULT 15
US-09-941-947A-19

```

; Sequence 19, Application US/09941947A
; Publication No. US20030003528A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Kofinas, Matheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odom, J. Martin
; APPLICANT: Picataggio, Steve
; APPLICANT: Rouviere, Pierre B.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941,947A
; CURRENT FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Methylobionas 16a
; US-09-941-947A-19

```

Alignment Scores:

```

Pred. No.: 1,03e-51 Length: 891
Score: 516.50 Matches: 113
Percent Similarity: 63.75% Conservative: 47
Best Local Similarity: 45.02% Mismatches: 88
Query Match: 35.55% Indels: 3
DB: 11 Gaps: 2

```

US-09-925-637-64 (1-287) x US-09-941-947A-19 (1-891)

```

Qy      23 LysSerValMetAspThrGlnLeuGlnLysSerMetLeuTyrSerLeuAsnAlaGlyGly 42
Db      76 GAAATATATCTGCCAACAACCTTGATCATCAGGCATCGCTATTCCTGATTGAAGCGCGC 135
Qy      43 LysArgIleArgProValLeuLeuLeuLeuLeuLeuLeuLeuAspSerLeuLeuThrGlyGlu 62
Db      136 AAACGACCCCGCGCTTGTGACTTATGCGACCGGTGACGCTTGGCGCTTGGCGGAAC 195
Qy      63 LeuGlyMetLysSerAlaIleAlaLeuGluMetIleHisThrTyrSerLeuIleHisAsp 82
Db      196 GTCTGGATCGCGCGCTTCGCGGTAATTCATCATGATGATTCGATTCACAGAC 255
Qy      83 AspleuPro1aMetAspAsnAspAspTyrArgArgGlyLysLeuThrAsnHisIleVal 102
Db      256 GATCTGCGCGCGCATGGAACAAGATGATGCGCGCGCAACCGAAGCTGTCAAGAGCT 315
Qy      103 TyGlyGlnThrPheAlaIleLeuAlaGlyAspAlaLeuLeuThrLysAlaPheGluLeu 122
Db      316 TACGACAGAGCCACCGCATTTTGGCGCGGACGCACTCAGGCGCTTGTGAAAGTT 375
Qy      123 IleSerSerAspAspArgLeuThrAspGlu-----ValLysIleLysValLeuGlnArg 140
Db      376 CTGGCCACAGACCCCGCATTCACGCTGCGCGCGCTGCGCTGAAATATGATCAGGCT 435
Qy      141 LeuSerIleAlaSerGlyHisValGlyMetValGlyGlyMetLeuAspMetGlnSer 160
Db      436 TACGACCCGCGCGCATGCTCAAGGATGTGGCGGTCAAGCCATCGATCTCGGCTCC 495
Qy      161 GluGlyGlnProIleAspLeuGlnThrLeuGluMetIleHisLysThrLysThrGlyAla 180
Db      496 GTGCGCGCGCAATTCAGCGTCCGCGAATCTGAAACATGATATCCACAGACTGGCGCC 555
Qy      181 LeuLeuThrPheAlaVal---MetSerAlaIleAspIleAlaAsnValAspAspThrThr 199
Db      556 CTGATCCGCGCGCATGCTGCGGCGATTCGCAACCCGATCTGATCTTGGCTC 615
Qy      200 LysGlnHisLeuGlnSerTyrSerTyrHisLeuGlyMetMetPheGlnIleLysAspAsp 219
Db      616 GCCAAGAACTGTGATCATATGCGCAATGCAATGAGCTTGTCTTCCAGGTCGCAAGCGAC 675
Qy      220 LeuLeuAspCysTyrGlyAspGluAlaLysLeuGlyLysValGlySerAspLeuGlu 239
Db      676 ATTTCTGACATTCGACAGCCGACCGGACACTGGCAAGACTCAGGCGAAGACATCGAT 735
Qy      240 AsnAsnLysSerThrTyrValSerLeuLeuGlyLysAspGlyAlaGlnAspLysLeuThr 259
Db      736 AACGACAAACCGACCTACCTCGGCTATTGGCATGGCTGGCCCAACAAAGCCGAC 795
Qy      260 TyrHisArgAspAlaAlaValAspGluLeuThr 270
Db      796 GAATTCACGAAACAGACATCGAAGCTTAACG 828

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Search completed: November 30, 2003, 07:55:56
Job time : 352 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:29:55 ; Search time 21 Seconds
(without alignments)
578,248 Million cell updates/sec

Title: US-09-925-637-64

Perfect score: 1453

Sequence: 1 MTNLPNKKLIDEVNNELSAVA.....ELTQIDEQNTKHLLEIVDL 287

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/aa/5A COMB pep: *
2: /cgn2_6/prodata/1/aa/5B COMB pep: *
3: /cgn2_6/prodata/1/aa/6A COMB pep: *
4: /cgn2_6/prodata/1/aa/6B COMB pep: *
5: /cgn2_6/prodata/1/aa/PCTUS COMB pep: *
6: /cgn2_6/prodata/1/aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	98.8	293	3	US-09-276-873-2
2	1015	69.9	302	4	US-09-134-001C-3171
3	657	45.2	297	1	US-08-534-910B-9
4	654	45.0	297	3	US-08-886-466-2
5	654	45.0	297	3	US-09-475-304-2
6	654	45.0	297	4	US-09-101-126-3
7	653	44.9	297	1	US-08-534-910B-7
8	650	44.7	297	1	US-08-534-910B-8
9	650	44.7	297	4	US-08-534-910B-10
10	650	44.7	297	4	US-09-367-528A-5
11	646	44.5	297	4	US-09-367-528A-1
12	645	44.4	297	1	US-08-534-910B-6
13	644	44.3	297	4	US-09-367-528A-3
14	551	36.7	291	4	US-09-275-742-2
15	533	37.9	312	4	US-09-107-532A-6724
16	521	35.9	393	3	US-09-187-050-34
17	520.5	35.8	393	3	US-09-187-050-2
18	520.5	35.8	393	3	US-09-187-050-14
19	520.5	35.8	393	3	US-09-187-050-16
20	520.5	35.8	393	3	US-09-187-050-18
21	520.5	35.8	393	3	US-09-187-050-20
22	520.5	35.8	393	3	US-09-187-050-22
23	520.5	35.8	393	3	US-09-187-050-24
24	520.5	35.8	393	3	US-09-187-050-26
25	520.5	35.8	393	3	US-09-187-050-27
26	520.5	35.8	393	3	US-09-187-050-28
27	520.5	35.8	393	3	US-09-187-050-29

28	520.5	35.8	393	3	US-09-187-050-30	Sequence 30, Appl
29	520.5	35.8	393	3	US-09-187-050-31	Sequence 31, Appl
30	520.5	35.8	393	3	US-09-187-050-32	Sequence 32, Appl
31	520.5	35.8	393	3	US-09-187-050-33	Sequence 33, Appl
32	517	35.6	285	3	US-09-187-050-12	Sequence 12, Appl
33	480	33.0	280	4	US-09-634-238-303	Sequence 303, Appl
34	474.5	32.7	401	4	US-09-252-991A-26387	Sequence 26387, A
35	465.5	32.0	377	4	US-09-420-211-2	Sequence 2, Appl1
36	442	30.4	308	4	US-09-328-352-4190	Sequence 4190, Ap
37	376.5	25.9	302	1	US-07-783-705A-1	Sequence 1, Appl1
38	346	23.8	298	1	US-08-095-726-4	Sequence 4, Appl1
39	346	23.8	298	1	US-08-096-043-4	Sequence 4, Appl1
40	346	23.8	298	1	US-08-093-577-4	Sequence 4, Appl1
41	346	23.8	298	1	US-08-096-623A-4	Sequence 4, Appl1
42	346	23.8	307	1	US-08-095-726-2	Sequence 2, Appl1
43	346	23.8	307	1	US-08-096-043-2	Sequence 2, Appl1
44	346	23.8	307	1	US-08-093-577-2	Sequence 2, Appl1
45	346	23.8	307	1	US-08-096-623A-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-09-276-873-2
; Sequence 2, Application US/09276873
; Patent No. 6107058
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael
; TITLE OF INVENTION: Ispra
; FILE REFERENCE: GM10208
; CURRENT APPLICATION NUMBER: US/09/276, 873
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-276-873-2

Query Match      98.8%; Score 1436; DB 3; Length 293;
Best Local Similarity 99.0%; Pred. No. 1.7e-132;
Matches 284; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTNLPNKKLIDEVNNELSAVAINKSVMDTQLEBSMLYSLNAGKRIRPVLLLTLDLSLNT 60
DB 1 MTNLPNKKLIDEVNNELSAVAINKSVMDTQLEBSMLYSLNAGKRIRPVLLLTLDLSLNT 60
QY 61 YELGKMSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKRYGWTAILAGDALLTKAF 120
DB 61 YELGKMSAIALEMHTYSLIHDDLPAMDNDYRRGKLTNNKRYGWTAILAGDALLTKAF 120
QY 121 ELISSDRLTDEKIKVLRSLASGHWGVMGQMDMSEGQIDLETLETHHKTGTGA 180
DB 121 ELISSDRLTDEKIKVLRSLASGHWGVMGQMDMSEGQIDLETLETHHKTGTGA 180
QY 181 LITFAVMSADIANDVDTTKEHLESYSYHIGMFFQIKDDLLDCYGDGAKKVGSDLEN 240
DB 181 LITFAVMSADIANDVDTTKEHLESYSYHIGMFFQIKDDLLDCYGDGAKKVGSDLEN 240
QY 241 NKSTYVSLGKDGAEKLTTHRDAAVDELTOIDQNTKHLLEIVDL 287
DB 241 NKSTYVSLGKDGAEKLTTHRDAAVDELTOIDQNTKHLLEIVDL 287

RESULT 2
US-09-134-001C-3171
; Sequence 3171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
```

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3171
LENGTH: 302
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3171

Query Match 69.9%; Score 1015; DB 4; Length 302;
Best Local Similarity 68.6%; Pred. No. 2,7e-91;
Matches 197; Conservative 41; Mismatches 49; Indels 0; Gaps 0;

QY 1 MTNLPMNKLIDEVNNELSVAINKSVMTQLEESMLYSINAGKRRIRPVLLLTIDSLNTE 60
DB 10 MKKLQNMKLIININTSLINKSIQSSPLKTNLEESMKYSINAGKRRIRPVLLLTIDSLNTE 69
QY 61 YELGMSAIALEMHTHTSLIHDLPAMDNDYRGRKLTNNKVGEMTALAGDALLTKAF 120
DB 70 YQGLSALALEMHTHTSLIHDLPAMDNDYRGRKLTNNKVGEMTALAGDALLTKAF 129
QY 121 ELISDRLTDEVYKIVLQRLSLASGHVGVGQMLDMOSEGQPIDLETLEMTHTKTA 180
DB 130 ELVSNPTTIDSVYSIKRLSKASGHLGVGQALDMESGKIRLETLESHETKTA 189
QY 181 LTRPAVMSADIANVDVDTKEHLESYSYHIGMMFOIKDILLDCYGEPAKLGKVGSLN 240
DB 190 LNFESVAAADIVIAQVEQNIKANKLDEFSHLGMMFOIKDILLDYGSESKLGKVGSDIVN 249
QY 241 NKSTYVSLGKQGAEDKLTTHRDAAVDELTDQIDQFNTKHLLEIVDL 287
DB 250 HKSTYVSLGKQGAEDKLTTHRDAAVDELTDQIDQFNTKHLLEIVDL 296

RESULT 3
US-08-534-910B-9
Sequence 9, Application US/08534910B
Patent No. 5766911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNUMA, Shinichi
APPLICANT: NAKAZAWA, Takeshi
APPLICANT: OGURA, Kyoza
APPLICANT: KOYAMA, Tanetsoshi
TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranylphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Tollenet, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-9

Query Match 45.2%; Score 657; DB 1; Length 297;
Best Local Similarity 47.7%; Pred. No. 2,7e-56;
Matches 133; Conservative 57; Mismatches 83; Indels 6; Gaps 2;

QY 1 MTNLPMNKLIDEVNNELSVAINKSVMTQLEESMLYSINAGKRRIRPVLLLTIDSLNTE 56
DB 1 MQLSVQPLNEKQXAVETALSYIRLEBPAKLTAKAMYSLEAGKRRIRPVLLLTIDSLNTE 60
QY 57 LNTVELGMSAIALEMHTHTSLIHDLPAMDNDYRGRKLTNNKVGEMTALAGDALL 116
DB 61 LGKDPVAGPVCAIMHTHTSLIHDLPAMDNDYRGRKLTNNKVGEMTALAGDALL 120
QY 117 TKAFELIS--SDRLTDEVYKIVLQRLSLASGHVGVGQMLDMOSEGQPIDLETLEMT 174
DB 121 TYAFQILTEIDBRIPSVRLRLERLAKVAGBQVVAQADMBESGKLTLSLEYTH 180
QY 175 KTKTGALLTPAVMSADIANVDVDTKEHLESYSYHIGMMFOIKDILLDCYGEPAKLGK 234
DB 181 RHTGMLQVSYAGALLGADARQTRREDEFRAHLGLFQIRDDITLDEBGEKIGKV 240
QY 235 GSDLENKSTYVSLGKQGAEDKLTTHRDAAVDELTDQID 273
DB 241 GSDSNKATYPALISLAGAKKELTFHIEAQRHLNAD 279

RESULT 4
US-08-886-466-2
Sequence 2, Application US/08886466C
Patent No. 6040165
GENERAL INFORMATION:
APPLICANT: Narita, Keiichi
APPLICANT: Ishida, Chika
APPLICANT: Takeuchi, Yoshie
APPLICANT: Ohno, Chikara
APPLICANT: Nishino, Tokuzo
TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
FILE REFERENCE: 77670/494
CURRENT APPLICATION NUMBER: US/08/886,466C
CURRENT FILING DATE: 1997-07-10
EARLIER APPLICATION NUMBER: JP 8-191635
EARLIER FILING DATE: 1996-07-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-08-886-466-2

Query Match 45.0%; Score 654; DB 3; Length 297;
Best Local Similarity 47.7%; Pred. No. 5,2e-56;
Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

QY 1 MTNLPMNKULIDEVNNELSAVINKSV---DTQLESMTLSNAGKRIIRPVLLITLDS 56
 Db 1 MAQLSVEQFLNEKQAVETALSRIERLEBPAKTKKAMAYSLBAGKRIIRPVLLITLSTVRA 60
 QY 57 LNTVEYLGKMSAIALEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 116
 Db 61 LGKDPVAGLPVACAIEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 120
 QY 117 TKAFLIS--SDRLTDEVKIKVLOSLASGHVGVGOMLMOSEGOPIDELETLEMH 174
 Db 121 TYAFQITEIDDERIPSVRLRIERLAKAAGEGVAGAAAMEBEGKTLTLESELYH 180
 QY 175 KTKTGALLTFPAVMSAADIANVDTTKEHLESYHIGMMFOIKODLLDCYGEBAKLGKV 234
 Db 181 RHKTGMLOYSVAGALLIGADARQTRREDEFPAHIGLAFQIRDDILIDEGAEKIGKPV 240
 QY 235 GSDLENNKSTYVSLGKDGAEKLTYYHRDAVDELTOID 273
 Db 241 GSDQSNKATYPALLSLAGAKKELAFHIEAQRHLNAD 279

RESULT 5
 US-09-475-304-2

/ Sequence 2, Application US/09475304

/ Patent No. 6225096

/ GENERAL INFORMATION:

/ APPLICANT: Nariita, Keishi

/ APPLICANT: Ishida, Chika

/ APPLICANT: Takeuchi, Yoshie

/ APPLICANT: Ono, Chikara

/ APPLICANT: Ohnuma, Shinichi

/ APPLICANT: Nishino, Tokuzo

/ TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE

/ FILE REFERENCE: 77670/494

/ CURRENT APPLICATION NUMBER: US/09/475,304

/ EARLIER FILING DATE: 1999-12-30

/ EARLIER APPLICATION NUMBER: JP 8-191635

/ EARLIER FILING DATE: 1996-07-03

/ NUMBER OF SEQ ID NOS: 9

/ SOFTWARE: Patentin Ver. 2.0

/ SEQ ID NO 2

/ LENGTH: 297

/ TYPE: PRT

/ ORGANISM: Bacillus stearothermophilus

/ US-09-475-304-2

Query Match 45.0%; Score 654; DB 3; Length 297;

Best Local Similarity 47.7%; Pred. No. 5, 2e-56;

Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

QY 1 MTNLPMNKULIDEVNNELSAVINKSV---DTQLESMTLSNAGKRIIRPVLLITLDS 56
 Db 1 MAQLSVEQFLNEKQAVETALSRIERLEBPAKTKKAMAYSLBAGKRIIRPVLLITLSTVRA 60
 QY 57 LNTVEYLGKMSAIALEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 116
 Db 61 LGKDPVAGLPVACAIEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 120
 QY 117 TKAFLIS--SDRLTDEVKIKVLOSLASGHVGVGOMLMOSEGOPIDELETLEMH 174
 Db 121 TYAFQITEIDDERIPSVRLRIERLAKAAGEGVAGAAAMEBEGKTLTLESELYH 180
 QY 175 KTKTGALLTFPAVMSAADIANVDTTKEHLESYHIGMMFOIKODLLDCYGEBAKLGKV 234
 Db 181 RHKTGMLOYSVAGALLIGADARQTRREDEFPAHIGLAFQIRDDILIDEGAEKIGKPV 240
 QY 235 GSDLENNKSTYVSLGKDGAEKLTYYHRDAVDELTOID 273
 Db 241 GSDQSNKATYPALLSLAGAKKELAFHIEAQRHLNAD 279

RESULT 6
 US-09-101-126-3

/ Sequence 3, Application US/09101126
 / Patent No. 6316216
 / GENERAL INFORMATION:
 / APPLICANT: ONO, CHIKARA
 / APPLICANT: NAKANE, HIROYUKI
 / APPLICANT: NISHINO, TOKUZO
 / APPLICANT: OHNUMA, SHINICHI
 / APPLICANT: HIROOKA, KAZUTAKE
 / TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
 / FILE REFERENCE: 77670/566
 / CURRENT APPLICATION NUMBER: US/09/101,126
 / EARLIER FILING DATE: 1999-04-27
 / EARLIER APPLICATION NUMBER: PCT/JP97/03921
 / EARLIER FILING DATE: 1997-10-29
 / EARLIER APPLICATION NUMBER: JP 8-307506
 / EARLIER FILING DATE: 1996-11-05
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO 3
 / LENGTH: 297
 / TYPE: PRT
 / ORGANISM: Bacillus stearothermophilus
 / FEATURE:
 / OTHER INFORMATION: 86-92 is an Asp-rich domain
 / US-09-101-126-3

Query Match 45.0%; Score 654; DB 4; Length 297;

Best Local Similarity 47.7%; Pred. No. 5, 2e-56;

Matches 133; Conservative 55; Mismatches 85; Indels 6; Gaps 2;

QY 1 MTNLPMNKULIDEVNNELSAVINKSV---DTQLESMTLSNAGKRIIRPVLLITLDS 56
 Db 1 MAQLSVEQFLNEKQAVETALSRIERLEBPAKTKKAMAYSLBAGKRIIRPVLLITLSTVRA 60
 QY 57 LNTVEYLGKMSAIALEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 116
 Db 61 LGKDPVAGLPVACAIEMHTYSLIHDDLPAMDNDYRGLTNHXYGGEWTAILADGALL 120
 QY 117 TKAFLIS--SDRLTDEVKIKVLOSLASGHVGVGOMLMOSEGOPIDELETLEMH 174
 Db 121 TYAFQITEIDDERIPSVRLRIERLAKAAGEGVAGAAAMEBEGKTLTLESELYH 180
 QY 175 KTKTGALLTFPAVMSAADIANVDTTKEHLESYHIGMMFOIKODLLDCYGEBAKLGKV 234
 Db 181 RHKTGMLOYSVAGALLIGADARQTRREDEFPAHIGLAFQIRDDILIDEGAEKIGKPV 240
 QY 235 GSDLENNKSTYVSLGKDGAEKLTYYHRDAVDELTOID 273
 Db 241 GSDQSNKATYPALLSLAGAKKELAFHIEAQRHLNAD 279

RESULT 7
 US-08-534-910B-7

/ Sequence 7, Application US/08534910B

/ Patent No. 5766911

/ GENERAL INFORMATION:

/ APPLICANT: KOIKE, Ayumi

/ APPLICANT: OBAI, Shusei

/ APPLICANT: NISHINO, Tokuzo

/ APPLICANT: OHNUMA, Shinichi

/ APPLICANT: NAKAZAWA, Takeshi

/ APPLICANT: OGURA, Kyoze

/ APPLICANT: KOYAMA, Tanetoshi

/ TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Kenyon & Kenyon

/ STREET: 1025 Connecticut Avenue, N.W., Suite 600

/ CITY: Washington

/ STATE: DC

/ COUNTRY: U.S.

/ ZIP: 20036-5405


```

ADDRESSER: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534, 910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-10

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Query Match          44.7%; Score 650; DB 1; Length 297;
Best Local Similarity 47.3%; Pred. No. 1,3e-55;
Matches 132; Conservative 55; Mismatches 86; Indels 6; Gaps 2;

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QY 1 MNTLPNKLIDEVNNELSVAINKSV---DTGLEESMLYSINAGKRIIPVLLLTDS 56
DB 1 MQLSVEQFLNEKQAVETALSRIERLEGPARKKAMAYSLEAGGRRIRPLLSTVQA 60
QY 57 LNTVEYLGMKSAFALAMHHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALL 116
DB 61 LGGDPVAVGVACATIEHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGL 120
QY 117 TFAFELIS--SDRLTDEVKIKVLQRLSIASGHVGVGGQMLDMOSEGQPIDLETLEM 174
DB 121 TYAFQILTEIDDRIPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTISELEYIH 180
QY 175 KRTYGALLTFVAVMSAADIANVDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKY 234
DB 181 RHHTGMLQGVAVAGALLIGADARQTRREIDFPAHLGLAFQIIRDDIIDLEGAEKIGKPV 240
QY 235 GSDLENNKSTYVSLGKDGAEKLTYHRDAVDELTOID 273
DB 241 GSDQNNKATYPPALLSLAGAKELAFHTEAQRHLRNAD 279

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RESULT 10
US-09-367-528A-5
Sequence 5, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA.
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367, 528A
PRIOR FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
NUMBER OF SEQ ID NOS: 6

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

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Query Match          44.7%; Score 650; DB 4; Length 297;
Best Local Similarity 49.6%; Pred. No. 1,3e-55;
Matches 134; Conservative 49; Mismatches 85; Indels 2; Gaps 1;

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QY 6 MNKLIDEVNNELSVAINKSVMDTGLEESMLYSINAGKRIIPVLLLTDSINTEYELGM 65
DB 10 LNEQQAQVETALSRIERLEGPARKKAMAYSLEAGGKRIIRPLLSTVRLALGKDPVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALLTFAFELIS- 124
DB 70 PVACAIEHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGLTYAFQILITE 129
QY 125 -SDRLTDEVKIKVLQRLSIASGHVGVGGQMLDMOSEGQPIDLETLEMHTKRTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTISELEYIHRKTKMLQ 189
QY 184 FAVMSAADIANVDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLENNKS 243
DB 190 YSVHAGALLIGADARQTRREIDFPAHLGLAFQIIRDDIIDLEGAEKIGKPVSDQNNKA 249
QY 244 TVVSLGKDGAEKLTYHRDAVDELTOID 273
DB 250 TYPALLSLAGAKELAFHTEAQRHLRNAD 279

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RESULT 11
US-09-367-528A-1
Sequence 1, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367, 528A
PRIOR FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
FEATURES:
NAME/KEY: PEPTIDE
LOCATION: 82
OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
US-09-367-528A-1

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Query Match          44.5%; Score 646; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 3,2e-55;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;

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QY 6 MNKLIDEVNNELSVAINKSVMDTGLEESMLYSINAGKRIIPVLLLTDSINTEYELGM 65
DB 10 LNEQQAQVETALSRIERLEGPARKKAMAYSLEAGGKRIIRPLLSTVRLALGKDPVGL 69
QY 66 KSAIALEMHTYSLIHDDLPAMDNDYRGRGLTNHXYGEMTALLADALLTFAFELIS- 124
DB 70 PVACAIEHTYSLIHDDLPAMDNDYLRGKPTNHKVFGEAMAILAGDGLTYAFQILITE 129
QY 125 -SDRLTDEVKIKVLQRLSIASGHVGVGGQMLDMOSEGQPIDLETLEMHTKRTGALLT 183
DB 130 IDDERIPPSVRLRIERLAKAAGPEGVAVAGQADMEGEGKTLTISELEYIHRKTKMLQ 189

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QY 184 FAVMSADIANVDDTTEHESYHLCGMFOIKDLDLCYGBAKLGGKVGSDLENKS 243
Db 190 YSVHAGALIGADARQTRREIDFPAHLGLAFQIRDDILDIEGAEEKIGKVGSDQSNKA 249
QY 244 TYVSLGKGADBDKLTYYHDAVDELTOID 273
Db 250 TYPALISLAGAKKLAFHIEAQRHLRNAD 279

RESULT 12
US-08-534-910B-6
Sequence 6, Application US/08534910B
Patent No. 5786911
GENERAL INFORMATION:
APPLICANT: KOIKE, Ayumi
APPLICANT: OBATA, Shusei
APPLICANT: NISHINO, Tokuzo
APPLICANT: OHNIMA, Shinichi
APPLICANT: MAKIZAWA, Takeshi
APPLICANT: OGURA, Kyoza
TITLE OF INVENTION: Mutated Farnesyl diphosphate Synthase Capable
TITLE OF INVENTION: Of Synthesizing Geranylgeranyl diphosphate And Gene Coding Ther
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: U.S.
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: IBM/Word Perfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,910B
FILING DATE: 28-SEPT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-25253
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)429-1776
TELEFAX: (202)429-0796
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
US-08-534-910B-6

Query Match 44.4%; Score 645; DB 1; Length 297;
Best Local Similarity 48.0%; Pred. No. 4e-55;
Matches 130; Conservative 56; Mismatches 79; Indels 6; Gaps 2;
QY 1 MNTLPMNKLDIVNNELSVAINKSVM---DTQLEBSMLYSINAGGKRIRPVLLLTLS 56
Db 1 MAOLSEQFNEKQAVETLSRIERLEGPALKKMAVSLGAGKRIRPVLLLTSTVRA 60
QY 57 LNTVEYLGKMSATALEMIHTSYSLIHDDLPAMNDNDYRGKLTNNKVVGEWTAIAGDAL 116
Db 61 LGKDPAVGLPVACALEMIHTSHLHDDLPAMDNDLRGRPTNNKVFGEWMAIAGDGL 120
QY 117 TKAFELIS--SDRLTDEVKIKVLRSLASGVHVGGMMLDMQSEGQPIDLETLEMIH 174

Db 121 TYAFOLITEIDRIPPSVRLRIERLAKAAGEGVAGQAAWMEGKTLTISELEYIH 180
QY 175 KTKTGALLTPAVMSADIANVDDTTEHESYHLCGMFOIKDLDLCYGBAKLGGKV 234
Db 181 RHKTGKQLQSVAGALIGADARQTRREIDFPAHLGLAFQIRDDILDIEGAEEKIGKPV 240
QY 235 GSDLENKSTYVSLGKGADBDKLTYYHDAVDELTOID 265
Db 241 GSDQSNKATYPALISLAGAKKLAFHIEAQRHLRNAD 271

RESULT 13
US-09-367-528A-3
Sequence 3, Application US/09367528A
Patent No. 6395525
GENERAL INFORMATION:
APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
TITLE OF INVENTION: Geranyl diphosphate Synthetase Gene
FILE REFERENCE: PH-586
CURRENT APPLICATION NUMBER: US/09/367,528A
CURRENT FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: JP97/346686
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 297
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-367-528A-3

Query Match 44.3%; Score 644; DB 4; Length 297;
Best Local Similarity 49.3%; Pred. No. 5e-55;
Matches 133; Conservative 49; Mismatches 86; Indels 2; Gaps 1;
QY 6 MNTLDEVNNEISVAINKSVMDTQLEBSMLYSINAGGKRIRPVLLLTLSINTERELGM 65
Db 10 LNEQKQAVETLSRIERLEGPALKKMAVSLGAGKRIRPVLLLTSTVRLKDPVGL 69
QY 66 KSAIALEMIHTSYSLIHDDLPAMNDNDYRGKLTNNKVVGEWTAIAGDALTKAFELIS- 124
Db 70 PVACALEMIHTSYSLIHDDLPAMDNDLRGRPTNNKVFGEWMAIAGDGLTYAFOLITE 129
QY 125 -SDRLTDEVKIKVLRSLASGVHVGGMMLDMQSEGQPIDLETLEMIHTKTKGALLT 183
Db 130 IDDERIPPSVRLRIERLAKAAGEGVAGQAAWMEGKTLTISELEYIHRRKTGMLQ 189
QY 184 FAVMSADIANVDDTTEHESYHLCGMFOIKDLDLCYGBAKLGGKVGSDLENKS 243
Db 190 YSVHAGALIGADARQTRREIDFPAHLGLAFQIRDDILDIEGAEEKIGKVGSDQSNKA 249
QY 244 TYVSLGKGADBDKLTYYHDAVDELTOID 273
Db 250 TYPALISLAGAKKLAFHIEAQRHLRNAD 279

RESULT 14
US-09-275-742-2
Sequence 2, Application US/09275742
Patent No. 6130069
GENERAL INFORMATION:
APPLICANT: Wilding, Edwina Imogen
APPLICANT: Gwynn, Michael
TITLE OF INVENTION: Ispra
FILE REFERENCE: GM10205
CURRENT APPLICATION NUMBER: US/09/275,742
CURRENT FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:32:20 ; Search time 31 Seconds
(Without alignments)
1707.568 Million cell updates/sec

Title: US-09-925-637-64
Perfect score: 1453
Sequence: 1 MTNLPNKKLIDVNNELSYA.....ELTQDEQNTKHLITVDL 287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues
Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1453	100.0	287	15	US-10-084-205-64
3	1442	99.2	293	9	US-09-815-242-12583
4	1415	97.4	288	9	US-09-815-242-5239
5	596	41.0	293	9	US-09-815-242-10630
6	549	37.8	291	9	US-09-815-242-13597
7	547	37.6	291	10	US-09-815-242-13273
8	516.5	35.5	297	10	US-09-934-903-14
9	516.5	35.5	297	10	US-09-934-868-72
10	516.5	35.5	297	11	US-09-941-947A-20
11	504.5	34.7	367	14	US-10-108-915-26
12	497.5	34.2	295	9	US-09-815-242-11239
13	494.5	34.0	350	14	US-10-108-915-22
14	487.5	33.6	369	14	US-10-108-915-18
15	485.5	33.4	299	9	US-09-815-242-10069

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	32.9	32.7	32.6	32.1	32.0	32.0	27.7	25.9	25.9	25.7	25.6	24.5	24.1	22.4	21.7	21.4	21.4	21.4	21.4	21.3	21.3	21.3	21.2	20.9	20.7	20.6	20.2	20.1	19.3	18.5	
	316	295	299	287	377	316	316	303	303	303	303	303	232	376	295	322	342	344	344	323	295	10	11	12	14	15	11	14	14	14	
	US-10-108-915-45	US-09-815-242-11971	US-09-815-242-14084	US-10-166-225A-159	US-09-934-778-2	US-10-108-915-16	US-10-108-915-20	US-09-941-947A-26	US-10-218-118-2	US-09-815-242-11382	US-09-815-242-11547	US-10-108-915-14	US-10-108-915-12	US-10-156-761-9190	US-10-166-225A-185	US-09-815-242-12603	US-10-108-915-38	US-09-815-242-10321	US-10-156-761-8668	US-09-815-242-13734	US-09-547-267-1	US-09-920-923-2	US-09-815-242-5315	US-10-156-761-10534	US-09-920-923-37	US-09-815-242-11142	US-10-108-915-30	US-09-815-242-12031	US-10-108-915-34		
	Sequence 45, Appl 1	Sequence 11971, A	Sequence 14084, A	Sequence 159, App	Sequence 2, Appl 1	Sequence 16, Appl 1	Sequence 20, Appl 1	Sequence 26, Appl 1	Sequence 2, Appl 1	Sequence 11382, A	Sequence 11547, A	Sequence 12, Appl 1	Sequence 12, Appl 1	Sequence 9190, App	Sequence 185, App	Sequence 12603, A	Sequence 38, Appl 1	Sequence 10321, A	Sequence 8668, App	Sequence 13734, A	Sequence 1, Appl 1	Sequence 2, Appl 1	Sequence 5315, App	Sequence 46, Appl 1	Sequence 10534, A	Sequence 37, Appl 1	Sequence 11142, A	Sequence 30, Appl 1	Sequence 12031, A	Sequence 34, Appl 1	

ALIGNMENTS

RESULT 1
US-09-925-637-64
Sequence 64, Application US/09925637
Patent No. US2002010338A1
GENERAL INFORMATION:
APPLICANT: ChOI
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/151,933
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-03
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 287
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-637-64
Query Match 100.0%; Score 1453; DB 10; Length 287;
Best Local Similarity 100.0%; Pred. No. 2.5e-139;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTNLPNKKLIDVNNELSYAIVKSYVDQTLKESMLYSLNAGKRRIRPVLLITLDSLNTE 60
DB 1 MTNLPNKKLIDVNNELSYAIVKSYVDQTLKESMLYSLNAGKRRIRPVLLITLDSLNTE 60
QY 61 YELGKSAIATLMTITVSLIHDLDLPAMDNDYRRGKLTNKKYGEWTAIADALTTKAF 120

```
Db      61 YELGMSAIALEMHTVSLIHDDLPMANDNDYRRGKLTNNKVGWETAIIAGDALLTKAF 120
Qy      121 ELISSDRLTDEVKIKVLRSLASGHVGVGQMLDMOSEGQPIDETLEMIHKTGTGA 180
Db      121 ELISSDRLTDEVKIKVLRSLASGHVGVGQMLDMOSEGQPIDETLEMIHKTGTGA 180
Qy      181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
Db      181 LITFAVMSAADIANVDDTTKEHLESYSYHLGMMFOIKDILLDCYGEBAKLGKVGSDLEN 240
Qy      241 NKSTYVSLGKGDAEDKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287
Db      241 NKSTYVSLGKGDAEDKLTTHRDAVDELTOIDQFNTKHLLEIVDL 287

RESULT 2
US-10-084-205-64
; Sequence 64, Application US/10084205
; Publication No. US20030049648A1
; GENERAL INFORMATION:
; APPLICANT: Choi Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB151P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 3.1
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-084-205-64

Query Match      100.0%; Score 1453; DB 15; Length 287;
Best Local Similarity 100.0%; Pred. No. 2,5e-139;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12583
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12583

Query Match      99.2%; Score 1442; DB 9; Length 293;
Best Local Similarity 99.3%; Pred. No. 3,4e-138;
Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5239
;; LENGTH: 288
;; TYPE: PRF
;; ORGANISM: Staphylococcus aureus
US-09-815-242-5239

Query Match 97.4%; Score 1415; DB 9; Length 288;
Best Local Similarity 99.3%; Pred. No. 1,8e-135;
Matches 280; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MNKLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSLNTVEYELGM 65
DB 1 MNKLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSLNTVEYELGM 60
QY 66 KSAIALEMIHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLTFAFELISS 125
DB 61 KSAIALEMIHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLTFAFELISS 120
QY 126 DRLTBEVKIKVLRSLIASGHVGMVGGQWLDMSQSPIDLTLEMIHTKTKGALLTFA 185
DB 121 DRLTBEVKIKVLRSLIASGHVGMVGGQWLDMSQSPIDLTLEMIHTKTKGALLTFA 180
QY 186 VMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGGKVGSDLENNKSTY 245
DB 181 VMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGGKVGSDLENNKSTY 240
QY 246 VSLGKGADKLTYHRDAVDELTOIDEOFTKHLLEIVDL 287
DB 241 VSLGKGADKLTYHRDAVDELTOIDEOFTKHLLEIVDL 282

RESULT 5
US-09-815-242-10630
;; Sequence 10630, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA 011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10630
;; LENGTH: 293
;; TYPE: PRF
;; ORGANISM: Enterococcus faecalis
US-09-815-242-10630

Query Match 41.0%; Score 596; DB 9; Length 293;
Best Local Similarity 46.0%; Pred. No. 3.4e-52;
Matches 134; Conservative 56; Mismatches 91; Indels 10; Gaps 5;

QY 1 MTNLPNN--KLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSLN 58
DB 1 MTNLPNN--KLIDEVNNELSVAINKSVMDTOLESMLYSINAGKRIKRPVLLLTLDLSLN 57
QY 59 TEYEL-GMSAIALEMIHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLT 117
DB 58 KEMETDQYVAASLEMIHTYSLIHDDLPAMDNDYRSGKLTNNKVGEMTAIILAGDALLT 117
QY 118 KAPFELISSDRLTDEYKIKVLRSLIASGHVGMVGGQWLDMSQSPIDLTLEMIHTKTK 177
DB 118 KAPFELISSDRLTDEYKIKVLRSLIASGHVGMVGGQWLDMSQSPIDLTLEMIHTKTK 176
QY 178 TGAULTFAVMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGGKVGSD 237
DB 177 TGAULTFAVMSAADIANDVDTTKEHLESYSYHLGMMFOIKDLDLDVCGDEAKLGGKVGSD 236
QY 238 LENNSTYVSLGKGADKLTY--HRDAVDELTOIDEOFTKHLLEIVDL 285
DB 237 LENNSTYVSLGKGADKLTY--HRDAVDELTOIDEOFTKHLLEIVDL 287

RESULT 6
US-09-815-242-13597
;; Sequence 13597, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA 011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13597

```
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13597

Query Match      37.8%; Score 549; DB 9; Length 291;
Best Local Similarity 46.2%; Pred. No. 2e-47;
Matches 121; Conservative 50; Mismatches 87; Indels 4; Gaps 3;

QY 28 TOLBSWLYSLNAGKRIKRPVLLLTLDLSLNTVEY-LGKMSAIALEMIHTYSLIHDDLP 86
DB 25 SSLRESVLYSIHAGKRIKRPVLLLEVEALQVATIKPAQAVALALEMIHTGSLIHDDLP 84
QY 87 MDDNDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDEKIKVLRSLASG 146
DB 85 MDDDDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDEKIKVLRSLASG 143
QY 147 HGVNAGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
DB 144 SLGVNAGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
QY 207 SYHGMFQIKDLDLCYGEBAKLGKVGSDLENNKSTYVSLGKGAEDKLTYHRDAV 266
DB 204 GELIGLAFQVRDVLDTVASFEIIGKTPQKDLQAEKSTYPALGLEESIAFCNQTLDOAN 263
QY 267 DELTOIDEQ--FNTKHLLEIVD 286
DB 264 EKLEIAQQLPFETESIVSVE 285

RESULT 7
US-09-815-242-13273
; Sequence 13273, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13273
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13273

Query Match      37.6%; Score 547; DB 9; Length 291;
Best Local Similarity 45.8%; Pred. No. 3.2e-47;
Matches 120; Conservative 50; Mismatches 88; Indels 4; Gaps 3;
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```
QY 28 TOLBSWLYSLNAGKRIKRPVLLLTLDLSLNTVEY-LGKMSAIALEMIHTYSLIHDDLP 86
DB 25 SSLRESVLYSIHAGKRIKRPVLLLEVEALQVATIKPAQAVALALEMIHTGSLIHDDLP 84
QY 87 MDDNDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDEKIKVLRSLASG 146
DB 85 MDDDDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDEKIKVLRSLASG 143
QY 147 HGVNAGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
DB 144 SLGVNAGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
QY 207 SYHGMFQIKDLDLCYGEBAKLGKVGSDLENNKSTYVSLGKGAEDKLTYHRDAV 266
DB 204 GELIGLAFQVRDVLDTVASFEIIGKTPQKDLQAEKSTYPALGLEESIAFCNQTLDOAN 263
QY 267 DELTOIDEQ--FNTKHLLEIVD 286
DB 264 EKLEIAQQLPFETESIVSVE 285

RESULT 8
US-09-934-903-14
; Sequence 14, Application US/09934903
; Patent No. US20020102690A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Mattheos
; APPLICANT: Odum, J. Martin
; APPLICANT: Schenzle, Andreas J.
; APPLICANT: No. US20020102690A1ton, Kelley C.
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Rouviere, Pierre
; APPLICANT: Piccataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
; FILE REFERENCE: C11646 US NA
; CURRENT APPLICATION NUMBER: US/09/934,903
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: September 1, 2001
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Methylobionas 16a
; FEATURE:
; OTHER INFORMATION: Amino acid sequences encoded by ORF7
US-09-934-903-14

Query Match      35.5%; Score 516.5; DB 10; Length 297;
Best Local Similarity 45.0%; Pred. No. 4.2e-44;
Matches 113; Conservative 47; Mismatches 88; Indels 3; Gaps 2;

QY 23 KSYMVDQLEBSMYSLNAGKRIKRPVLLLTLDLSLNTVEYELGKMSAIALEMIHTYSLIH 82
DB 26 ENILPQTHQAMKYSVLNAGKRIKRPVLLTYATGALGPENVLDAACAAVEFIHVSILHD 85
QY 83 DLPRAMNDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDE--VKIKVLR 140
DB 86 DLPRAMNDYRGRKLTNNKRYGEMWTAILAGDALITKAFELISSDRDLTDE--VKIKVLR 145
QY 141 LSIASGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
DB 146 LSIASGQVLDMEGEHQHLSLEELQTHANKTGTLAVPQAAAIILSPENQVRLKTV 203
QY 200 KEHLESYVHLMGMPQIKDLDLCYGEBAKLGKVGSDLENNKSTYVSLGKGAEDKLT 259
DB 206 AKKLDHYAKTIGLSFQVKDILDLIDVATLTGKQKIDIDNDKPYPALGMAKQKQAO 265
QY 260 YHRDAVDEL 270
DB 260 YHRDAVDEL 270
```

Db 266 ELHEQAVESLT 276

RESULT 9

US-09-934-868-72

Sequence 72, Application US/09934868

Patent No. US20020137190A1

GENERAL INFORMATION:

APPLICANT: Koffas, Matheos

APPLICANT: Odom, James M

APPLICANT: Schenle, Andreas J

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: C11596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

SOFTWARE: Microsoft Office 97

SEQ ID NO 72

LENGTH: 297

TYPE: PRT

ORGANISM: Methylobionas 16a

FEATURE:

OTHER INFORMATION: Amino acid sequences encoded by ORF7 - ISPa

US-09-934-868-72

Query Match 35.5%; Score 516.5; DB 10; Length 297;

Best Local Similarity 45.0%; Pred. No. 4.2e-44;

Matches 113; Conservative 47; Mismatches 88; Indels 3; Gaps 2;

QY 23 KSVMDTQLEESMLYSINAGKRIKRPVLLTLTDSINTEVELGKMSAIALEMHTYSLIHD 82

DB 26 ENLIPOTLQAMKRYSTLNGKRRPRLTYATGALGPENVLDAPACAVFHVYSLLIHD 85

QY 83 DLPAMDNDYRRGKLTNNKRYGEMTALILAGDALITKAFELISSDDLRTDE--VKIKYLOR 140

DB 86 DLPAMDNDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGITVDAPARLKMITA 145

QY 141 LSTASGHVGMVGOMLDMOSGQPIDLETLEMHTKTKGALLTFAY-MSAADIANVDTT 199

DB 146 LTPASGSGQWVGQALDLSVGRKLTLPBLENMHIHTGALLIRASVNLALSKPDLDTCV 205

QY 200 KEHLIESYHLGMMFQIKDLDLCYGEAKLGRKVSDENNKSTYVSLGKGAEDKLT 259

DB 206 AKLDHYAKCIGSFVKDIDLEADTATLGKQKIDNDKPTYPALLGMAGAKQKQ 265

QY 260 YHRDAVDEL 270

DB 266 ELHEQAVESLT 276

RESULT 10

US-09-941-947A-20

Sequence 20, Application US/09941947A

Publication No. US20030003528A1

GENERAL INFORMATION:

APPLICANT: Brzostowicz, Patricia C.

APPLICANT: Cheng, Qiong

APPLICANT: DiCosimo, Deana J.

APPLICANT: Koffas, Matheos

APPLICANT: Miller, Edward S. Jr.

APPLICANT: Odom, J. Martin

APPLICANT: Picatagallo, Steve

APPLICANT: Rouviere, Pierre E.

TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

FILE REFERENCE: C11903 US NA

CURRENT APPLICATION NUMBER: US/09/941,947A

CURRENT FILING DATE: 2001-09-01

PRIOR APPLICATION NUMBER: 60/229,907

PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Microsoft Office 97

SEQ ID NO 20

LENGTH: 297

TYPE: PRT

ORGANISM: Methylobionas 16a

US-09-941-947A-20

Query Match 35.5%; Score 516.5; DB 11; Length 297;

Best Local Similarity 45.0%; Pred. No. 4.2e-44;

Matches 113; Conservative 47; Mismatches 88; Indels 3; Gaps 2;

QY 23 KSVMDTQLEESMLYSINAGKRIKRPVLLTLTDSINTEVELGKMSAIALEMHTYSLIHD 82

DB 26 ENLIPOTLQAMKRYSTLNGKRRPRLTYATGALGPENVLDAPACAVFHVYSLLIHD 85

QY 83 DLPAMDNDYRRGKLTNNKRYGEMTALILAGDALITKAFELISSDDLRTDE--VKIKYLOR 140

DB 86 DLPAMDNDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGITVDAPARLKMITA 145

QY 141 LSTASGHVGMVGOMLDMOSGQPIDLETLEMHTKTKGALLTFAY-MSAADIANVDTT 199

DB 146 LTPASGSGQWVGQALDLSVGRKLTLPBLENMHIHTGALLIRASVNLALSKPDLDTCV 205

QY 200 KEHLIESYHLGMMFQIKDLDLCYGEAKLGRKVSDENNKSTYVSLGKGAEDKLT 259

DB 206 AKLDHYAKCIGSFVKDIDLEADTATLGKQKIDNDKPTYPALLGMAGAKQKQ 265

QY 260 YHRDAVDEL 270

DB 266 ELHEQAVESLT 276

RESULT 11

US-10-108-915-26

Sequence 26, Application US/10108915

Publication No. US20020177204A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Shen, Jennie

APPLICANT: Williams, Mark

TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases

FILE REFERENCE: B01286 US NA

CURRENT APPLICATION NUMBER: US/10/108,915

CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592

PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Microsoft Office 97

SEQ ID NO 26

LENGTH: 367

TYPE: PRT

ORGANISM: Glycine max

US-10-108-915-26

Query Match 34.7%; Score 504.5; DB 14; Length 367;

Best Local Similarity 44.1%; Pred. No. 9.5e-43;

Matches 116; Conservative 42; Mismatches 96; Indels 9; Gaps 3;

QY 20 AINKSYMDT-----QLEESMLYSINAGKRIKRPVLLTLTDSINTEVELGKMSAIALE 72

DB 86 AVNKALDDVAVSREPQKIHENKRYSLLAGGKRRPVLCAACGLVGEEETAPAPACALE 145

QY 73 MHTYSLIHDDLPAMDNDYRRGKLTNNKRYGEMTALILAGDALITKAFELISSDDLRTDE 132

DB 146 MHTYSLIHDDLPAMDNDLRRGKPTCHKAYDEATAILAGDALQALAFEVLANDPGITVDAPARLKMITA 145

QY 133 VKI-KYLORLSTASGHVGMVGOMLDMOSG-QPIDLETLEMHTKTKGALLTFAYMSAA 190

DB 206 GRIVRAIGELARSIGSGVAGQVVDINSEGLADVLERLEFHVHTKTAALLEGAVVLGA 265

QY 191 DIANVDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNKSTYVSLIG 250
DQ 266 ILGGSTDEVEKLRKRFARVIGLLFQVVDLIDVTKSSQELGKTAQKDLVADKTYPRLLG 325
QY 251 KQGAEDKLTYYHDAVDELTOID 273
DQ 326 IEKSKVFAAKLNKADQDLGVGFD 348

RESULT 12

US-09-815-242-11239
Sequence 11239, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyckind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,991
PRIOR FILING DATE: 2000-12-32
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11239
LENGTH: 295
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-11239

Query Match 34.2%; Score 497.5; DB 9; Length 295;
Best Local Similarity 41.0%; Pred. No. 3.5e-42;
Matches 116; Conservative 52; Mismatches 100; Indels 15; Gaps 4;

QY 16 ELASVINKSVMDTLE-----ESMYSLNAGSKRIRPVLLLTLDLSLNTVEYELGM 65
DQ 10 QVQTRIR-FLAQFEGIESHNAPLEAMKVALLGKRVPRPVATGMLGAEKXTLD 68
QY 66 KSAIALEMITYSLIHDDLPAMDNDYRKGKLTNKKYGGWTAILAGDALLTAFAELISS 125
DQ 69 YAAAAIHAHAYSIHDDLPAMDNDNRGHPCHIOFDEATAILADALQSAFAFELITK 128
QY 126 DDLRLDVKIKVLRSLASGAVGVGOMLDMQSEOPIDLETLEMHHKTKGALLTFA 185
DQ 129 TPNISTQKALTIQLAQAGVQGMCLGQSLDLISHKQISLSELEIHHKTKGALL-IA 187
QY 186 VMSAADIAN--VDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNK 242
DQ 188 ALKAGFCSHFTDKREGSLYQAAEAGLAFQVQDDILIDEGSASIEGQVAGADLDLQ 247
QY 243 STYVSLIGKQGAEDKLTYYHDAVDELTOIDEGNTTHLEIV 285
DQ 248 STYPRKLLIGLGAKQKADLVYASLSELEKIPDTTYALAEFI 290

RESULT 13

US-10-108-915-22
Sequence 22, Application US/10108915
Publication No. US20020177204A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Shen, Jennie
APPLICANT: Williams, Mark
TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
FILE REFERENCE: BBI286 US NA
CURRENT APPLICATION NUMBER: US/10/108,915
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592
PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Microsoft Office 97
SEQ ID NO 22
LENGTH: 350
TYPE: PRT
ORGANISM: Glycine max
US-10-108-915-22

Query Match 34.0%; Score 494.5; DB 14; Length 350;
Best Local Similarity 43.3%; Pred. No. 9.2e-42;
Matches 114; Conservative 42; Mismatches 98; Indels 9; Gaps 3;

QY 20 AINKSVMDT-----QLESMLYSINAGSKRIRPVLLLTLDLSLNTVEYELGMSAIALE 72
DQ 69 AVNKGDDSVSLNEPKKIHAMRYSLLAGSKRVPRVLCVAAGLVGHGHEATAPACALE 128
QY 73 MHTTSLIHDDLPAMDNDYRKGKLTNKKYGGWTAILAGDALLTAFAELISSDDRLTDS 132
DQ 129 MHTMSLIHDDLPAMDNDYRKGKPTNHTVFGEDVAVLADALLAFEFHIAASTRGASA 188
QY 133 VKI-KVLRSLASGAVGVGOMLDMQSEG-OPIDLETLEMHHKTKGALLTFAVMSAA 190
DQ 189 PRLRAIGELARSIGSEGLAVGVVDINSBGLADVGLERLEFTHHKTALLGCAVVLGA 248
QY 191 DIANVDDTTKEHLESYSYHLGMMFOIKDLDLCYGBEAKLGGKVVGSDDLNNKSTYVSLIG 250
DQ 249 ILGGSTDEVEKLRKRFARVIGLLFQVVDLIDVTKSSQELGKTAQKDLVADKTYPRLLG 308
QY 251 KQGAEDKLTYYHDAVDELTOID 273
DQ 309 IEKSKVFAAKLNKADQDLGVGFD 331

RESULT 14

US-10-108-915-18
Sequence 18, Application US/10108915
Publication No. US20020177204A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Shen, Jennie
APPLICANT: Williams, Mark
TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
FILE REFERENCE: BBI286 US NA
CURRENT APPLICATION NUMBER: US/10/108,915
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592
PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 369
TYPE: PRT
ORGANISM: Glycine max
US-10-108-915-18

Query Match 33.6%; Score 487.5; DB 14; Length 369;
Best Local Similarity 44.9%; Pred. No. 5,1e-41;
Matches 111; Conservative 43; Mismatches 88; Indels 5; Gaps 4;

QY 13 VNNELSVAINKSVMDT-QLEESMLYSINAGKRIKRPVLLLTLDLSINTEYELGMKSAIAL 71
DB VNQALDPAAL--ALRDPKRIHQAMRYSILLAGKKEVRPLCIAACELVGTEATAIIPAAAV 146
QY 72 EMHTHTSLIHHDDLPAANDNDYRRGKLTNNKVGEMTALLAGDALITKAFELISSDDL 130
DB 147 EMHTHTSLIHHDDLPCMDNDLRRGKPTNNKVGEDVAVLADLALPAPFHVAASTEGVS 206
QY 131 DEKIKLQRLSLASGSHVGMVGMQMLDMQSEG-QPIDLETLFEMIHKTKTGALLTFVMSA 189
DB 207 PSRVVAIGELASITGEGVLAQVVDIDSEGVANGLFTLETHAKTALAEAAVVG 266
QY 190 ADIANVDDTTKEHLESYSYHLGMMFOIKDDLDCTGDEAKLGKVSDELENNKSTYVSL 249
DB 267 AIVGGSDSEVEKLRKFRARCIGLLFQVVDLIDVTSSEELGTAGKDLVADKVTYPKLL 326
QY 250 GKGGAED 256
DB 327 GIDKSKE 333

RESULT 15
US-09-815-242-10069
; Sequence 10069, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zysskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10069
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10069

Query Match 33.4%; Score 485.5; DB 9; Length 299;
Best Local Similarity 41.8%; Pred. No. 6e-41;
Matches 118; Conservative 42; Mismatches 117; Indels 5; Gaps 4;

QY 10 IDEVNNELSVAINK-SYMDTQLESMLYSINAGKRIKRPVLLLTLDLSINTEYELGMKSA 68
DB 11 VKQANQALSRFIALPFPQNTPVVETWQYGLLGGKRLRPLVATGMFVSTNTLDAPA 70

QY 69 IALEMHTHTSLIHHDDLPAANDNDYRRGKLTNNKVGEMTALLAGDALITKAFELISSDDL 127
DB 71 AAVECHIAVSLIHHDDLPAANDDDLRGLPTCHVKKEBANAILAGDALQTLAPSLSDADM 130
QY 128 -RLTDEVKIKVLQRLSLASGSHVGMVGMQMLDMQSEGQPIDLETLFEMIHKTKTGALLTFV 186
DB 131 PEVSDRDRISMISELASAGIAGMCGQALDIDABGKHVPLDALERIHHKTKGALLIRAAV 190
QY 187 -MSADIANVDDTTKEHLESYSYHLGMMFOIKDDLDCTGDEAKLGKVSDELENNKSTY 245
DB 191 RLGALISAGDKGRRALPVLDKYAESIGLAFQVDDLIDVVDATLTKRGQADQOLGKSTY 250
QY 246 VSLGKGGAEDKLTYYRDAAVDELQIDEGQ-FNTKHLLEIVD 286
DB 251 PALGLGQARKKARLDLIDAROSLQJLABQSIDTSALALAD 292

Search completed: November 26, 2003, 15:37:47
Job time : 31 secs

